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Listing first 45 summaries
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ALIGNMENTS

AAYE	AAY87461
Ü	AAY87461 standard; peptide; 12 AA.
A X	AAY87461;
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X D	03-JUL-2000 (first entry)
DE	Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3.
×	
ΧW	Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB;
Κ¥	
¥	adjuvant; immune disorder; diarrhoea.
SO	Vibrio cholerae.
SO X	Escherichia coli.
PN	WO20014114-A1
XX	HOROCOTALLY Dr.
X PD	16-MAR-2000.
X PF	07-SEP-1999; 99WO-GB02970.
PR	07-SEP-1998; 98GB-0019484.
PA	(UYBR-) UNIV BRISTOL.
r X	Williams NA, Hirst TR;
DR X	WPI; 2000-256943/22.
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PT PX R

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous

Disclosure; Page 15; 62pp; English.

GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AX87460-Y87463 particularly preferred.

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Query Match Best Local

Sequence

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DB 21; L. 4.6e-05; 0;

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therapy.

Sequence

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B

oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for :

immuno-

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RESULT 2
AAP93498
 ₽
This sequence corresponds subunit. The DNA sequence
                                                New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn. of antibodies.
                                                                                         WPI; 1989-356496/48.
N-PSDB; AAN92414.
                                                                                                                                          (PRAX-)
                                                                                                                                                                                                                                                   CTP3 epitope of Cholera toxin B subunit; flagellin vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                  CTP3 epitope of
                                                                                                                                                                                                                                                                                                       03-MAY-1990
                             Disclosure; fig.4B; 137pp; English
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LEYLAND STANDFORD JUI
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                                                                                                                                                                                                                                                                                 the Cholera toxin B subunit.
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                                                                                A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85125-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                        Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified aldehyde silica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR85125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR85125 standard; peptide; 15
                                                  Sequence
                                                                         secretory
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                                                                                                                                                                                                                                                                   WPI; 1995-403805/51.
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                                                                                                                                                                                                                                                                                                                                                             cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB end/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
                                                                                                                                                                                                                                                                                    represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunomodulators and for treating diarrhea glycolipid receptor {\tt GM-1} -
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams NA,
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              facilitate the entry of subunit A into the host cell via the binding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYBR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200014114-A1
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1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-256943/22
                                                                                                                         l Similarity
12; Conserv
                                                                                                                                                                                                                                                21 AA;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0019484
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                                                                                                                                                      100.0%;
                                                                                                                         0;
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                                                                                                                                                   Score 62; DB 21;
Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                Length 21;
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO:4
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i the
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RESULT 5
AAY87463
ID AAY8

AAY87463 standard; peptide; 21 AA.

18-MAR-1996

(first entry)

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RESULT 6
AAR76748
ID AAR7
XX
AC AAR7
XX
DT 18-M
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                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                              The invention relates to peptide fragments of the Escherichia coli heat C labile enterotoxin (Etx) and its closely related homologue, cholera coxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are C composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, while the B subunits (EtxB and CtxB) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/or CtxB, exerting the same effects as CC mormal EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC Therefore, the peptides may be used in the production of a composition immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 CC represent preferred peptides of the invention, AAY87480 being
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor {\tt GM-1} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside readjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E. coli heat labile enterotoxin B-derived peptide,
                                   AAR76748;
                                                                   AAR76748 standard; Protein;
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                              particularly preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY87463;
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                                                                                                                                                       σ
                                                                                                                                                                                        1 VEVPGSQHIDSQ 12
                                                                                                                                                       VEVPGSQHIDSQ 17
                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                          100.0%;
                                                                     23
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                          Score 62; DB 21;
Pred. No. 8.6e-05;
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                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                          0,
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                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                          Gaps
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AAP30265
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                                                                               20
                                                                                                                                                                                            This sequence is encoded by a fragment of the plasmid plPA93

CW which was used in the production of finh fusion genes comprising

the cholera toxin B subunit inserted into the finh gene. This insert

CC shows the inclusion of the B subunit into the Finh protein at position

CC 24-226. The chimeric genes were then opt. further modified by insertion

CC of the hepatitis B virus surface antigen pre-S2 region into a different

CC position of the Finh adhesin of type I finbriae. Restiction site handles

CC (BglII-sites) were introduced into the finh gene, and the foreign

CC epitopes are then inserted in-frame. In the selected positions the

CC insertion of the epitopes did not significantly alter the adhesive

CC function of the Finh protein. The expression of the chimeric proteins

CC of using bacterial adhesins as general presenters of foreign antigens and

CC epitopes. These chimeric genes may be used in the production of variant

Finh adhesins which may be useful for targetting active compounds
                                                                                                         Matches
                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FimH;
FimA;
   AAP30265
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ93061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-275442/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hasty DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                             compounds and microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GXBI-)
                                                                                                       Local Similarity
nes 12; Conser
                                                                                ш
                                                           u
                                                                                                                                                                            adhesins bind
                                                                                                                                                                                       microbial
                                                        VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type :
FimF;
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S
                                                                                                                                                                                                                                                                                                                                                                                                            specific bacterial adhesins - uses and microbial cells to locations
  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klemm
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Escherichia coli
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FimG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fimbriae; organelle; adhesin; alpha-D-mannoside residue;
                                                                                                                                                     A,
                                                                                                                                                                                       cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0187166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-DK00042
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5..19
/note=
20..22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholera toxin B subunit and FimH 224-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
  Protein;
                                                                                                                                                                                       ç
                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molin S,
                                                                                                                                                                                      locations comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Represents FimH residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Represents FimH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Linker peptide"
                                                                                                                             .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding site;
   26
                                                                                                       0;
                                                                                                                  Score 62;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pallesen
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxin B
                                                                                                                                                                                                                                                                                                                                                                                                             useful
ions of
                                                                                                     DB 16;
. 9.6e-05;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit 50-64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR;
                                                                                                                                                                                       selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sokurenko
                                                                                                                                                                                                                                                                                                                                                                                                             for targetting receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplify; ss
                                                                                                                            Length 23;
                                                                                                       Indels
                                                                                                                                                                                      receptors to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΕV
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                                                                                                                                                                                                                                                                                                                                                                                                                        active
                                                                                                      Gaps
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RESULT 8
AAP50439
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                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                    and vaccination against, choirs infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B, sub-unit polypeptide(s) as vaccines medicaments - effective against Escherichia coli and cholerae infections, are prepd. by solid phase pepti
                               Synthetic
                                                                                                           01-JAN-1980
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                    The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixithese toxins to cell walls. The peptides are used in the treatment of,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of amino acids 50\text{-}75 of the carries an Arg at posns. 67 and 73.
                                                     Heat-labile
                                                                         Network polymer 
labile toxin (L:
                                                                                                                                 AAP50439;
                                                                                                                                                      AAP50439 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS ) CNRS CENT NAT RECH SCI. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-1983
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                                                                                                                                                                                                                       1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1983-834645/49
                                                                                                                                                                                                            VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                  26 AA;
                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative
                                                     enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raulais D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                          (first entry)
                                                                        er which comprises a series (LT)/heat-stable toxin (ST)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82FR-0009167
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                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rivaille P,
                                                                                                                                                                                                                                                                             .0%;
                                                                                                                                                       41
                                                                                                                                                                                                                                                       0;
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Pred. No.
                                                                                                                                                       A
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                                                                        of composite polypeptide r
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                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide synthesis
                                                                                                                                                                                                                                                                           Length 26;
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Vibrio
                                                                         repeating
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized cys residu of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys. X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cy of the repeating units. This polypeptide may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic polypeptide(s) for puseful for vaccination of mammals
                                                                    useful
                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                            Network polymer which comprises a series of composite E. coli heat-
labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating unti
                                                                                                                                                                                                                                                                                                                                                                                           AAP50436 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghten RA
                                                Claim
                                                                    New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                        WPI;
                                                                                                                            Houghten
                                                                                                                                                  (SCRI-)
                                                                                                                                                                         12-DEC-1983;
                                                                                                                                                                                               12-DEC-1984;
                                                                                                                                                                                                                      20-JUN-1985
                                                                                                                                                                                                                                           WO8502611-A
                                                                                                                                                                                                                                                                                        Heat-labile enterotoxin;
                                                                                                                                                                                                                                                                                                                                                01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                       AAP50436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-DEC-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEVPGSQHIDSQ
                                                                                                     1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1985-159230/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Page 100; 120pp; English.
                                                                                                                                                  SCRIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                              100; 120pp; English.
                                                                                                                                                                         83US-0559469
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                                                                                                                                                  CLINIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                      heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                             46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 6;
Pred. No. 0.00018;
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s against the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli enterotoxin(s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 41;
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              Cys residues
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VEVPGSQHIDSQ

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VEVPGSQHIDSQ 12

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RESULT 10
AAP30600
Query Match
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Best Local
                                                                              administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                      (CNRS )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of amino carries an Arg at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination of mammals for protection against the enterotoxins. composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                             Cholera toxin medicaments -
                                                                                                                                                                                                                                                                              WPI; 1983-834645/49
                                                           Sequence
                                                                                                                             and vaccination against, cholera infections and animal and human infections due to {\tt E.} coli (enterotoxin LT). The medicament may l
                                                                                                                                                     these toxins
                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                 cholerae infections, are prepd.
                                                                                                                                                                                                                                                                                                     Guyongruaz A,
                                                                                                                                                                                                                                                                                                                   Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                               EP95426-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP30600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VEVPGSQHIDSQ 12
                                                                                                                                                 inventors claim cholera toxin B1 subunit sequences which carry in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have wn that Arg in posns. 35, 67 and 73 play an important role in fixing se toxins to cell walls. The peptides are used in the treatment of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVPGSQHIDSQ
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12; Conser
                                                                                                                                                                                                                                                                                                                                       CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                           Page
                                                           47
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         100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                 Raulais D,
                                                                                                                                                                                                                                                                                                                                         PASTEUR.
                                                                                                                                                                                                                                                                                                                                                   CENT NAT RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                               B, sub-unit polypeptide(s) as vaccines
effective against Escherichia coli and
ctions, are prepd. by solid phase peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۸,
                                                           Ä
                                                                                                                                                                                                          11; 13pp;
                                                                                                                                                                                                                                                                                                     Delmas
                                                                                                                                                                                                                                                                                                                                                                          82FR-0009167
                                                                                                                                                                                                                                                                                                                                                                                                 83EP-0401052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 posns.
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                                                                                                                                                                                                            French.
                                                                                                                                                                                                                                                                                                                   Rivaille P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350-75 of the cholera . 35, 67 and 73.
                      .0%;
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            Score 62; DB Pred. No. 0.0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                 solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                   Siffert O,
                         0.00021;
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0.00021;
                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxin B1 subunit which
                                  Length 47;
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AAR72545
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Best Local
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                   information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
ADP-ribosylating toxin; three-dimensional struct
                            Escherichia coli verotoxin-1 B-subunit.
                                               08-DEC-1999
                                                                  AAY41816;
                                                                                    AAY41816
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                      AAR72540-R72545 are structurally equivalent B-subunits ADP-ribosylating toxins, pertussis holotoxtin (PT), E. labile toxin (LT), and verotoxin-1 (VT). The structural
                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                       New modified forms of pertussis holotoxin acrystalline forms of pertussis holotoxin a
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-132623/18
                                                                                                                                                                                                                                                                                                                                                                                     Oomen
                                                                                                                                                                                                                                                                                                                                                                                             Armstrong
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31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72545 standard;
                                                                                                                                                                                                                             pertussis
                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP-ribosylating toxin (verotoxin-1 B-subunit)
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                                                                                                                                                                       Local Similarity
les 12; Conser
                                                                                                                                                    1 VEVPGSQHIDSQ 12
                                                                                                                                   VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                molecules
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                                                                                    standard;
                                                                                                                                                                                                                             infection.
                                                                                                                                                                                                                                                                                                                                                                                    GD, Cockle SA,
Read RJ, Stein
                                                                                                                                                                                                           93 AA;
                                                                                                                                                                       Conservative
                                             (first entry)
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94US-0251121.
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 structure;
                                                                                                                                                                                                                                                                                                           54pp;
                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                     Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                              100.
         PT;
                                                                                                                                                                               .0%;
                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                    Hazes B, PE;
crystalline pertussis holotoxin;
; LT; immunoprotective; infection.
                                                                                     93
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                                                                                                                                                                      Score 62; DB
Pred. No. 0.0
0; Mismatches
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0.00045;
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AAW95226
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
             Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read RJ,
Hazes B,
                                                                               E. coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:

(1) identification of at least one amino acid (aa) residue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
heat-labile;
                                                                                                               16-MAR-1999
                                                                                                                                              AAW95226;
                                                                                                                                                                            AAW95226 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New method for producing modified
                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
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                                                                                                                                                                                                                                                                              1 VEVPGSQHIDSQ
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Oomen RP;
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                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative (
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H
                                                                                                             (first entry)
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                            51
                                                                             toxin (LT) beta-subunit sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                          Score 62;
Pred. No.
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. 0.00045;
ches 0;
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                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                         93;
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                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 14
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ID AAY68
XX AAY68
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XX Pertu
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KW dipht
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying CC at least 1 site in a PT that interacts with a molecule that is capable of CC forming a complex with the holotoxin and which molecule is an effector CC molecule which is an adenine nucleotide and which site contributes to CC toxicity, cell binding or enzymatic activity of PT. The functional CC interacting site(s) are identified by analysing the three dimensional CC structure of crystalline PT, determined by X-ray crystallogaphy. The CC identified interacting site(s) are modified to alter toxicity, cell CC binding or enzyme activity of the PT. The methods can be used to alter a CC biological activity such as toxicity, enzymatic activity, mitogenicity, CC cell binding and adjuvanticity of the PT. The three-dimensional structure CC of PT have functional and/or structural resemblance to other bacterial CC toxins such as diphtheria toxin (PT), Pseudomonas exotoxin A (ETA), the CC heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present CC sequence represents the beta-subunit of LT toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local !
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                             Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                               AAY68365;
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                             25-JAN-2000
                                                                          US6018022-A
                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                               17-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY68365 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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12; Conserv
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                                                                                                                                                                                                          crystal
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                                                                                                                                                                                                                                                                                                             toxin
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                                                                                                                                                                                                                                                                                                                                                               (first
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                             structure;
                                                                                                                                                                                                                                                                                                             subunit
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                                                                                                                                                                                                          X-ray
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                                                                                                                                                                                                                                                                                                             NO:26
                                                                                                                                                                                                       crystallography;
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RESULT 15
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Best Local
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                                 22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read RJ,
Hazes B,
                                                                                                         02-JAN-2001
                                                                                                                                                                                                                                 E coli verotoxin-1 B subunit
                                                                                                                                                                                                                                                           03-APR-2001
                                                                                                                                                                                                                                                                                                           AAB66239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crystalline form of proteins which have
                                                                                   21-MAY-1998;
                                                                                                                                 US6168928-B1
                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                         Pertussis toxin; crystal structure; whooping cough; biological activity;
                                                                                                                                                                                                                                                                                   AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                 islet-activating protein.
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                                                                                                                                                                                             ymphocytosis-promoting factor; histamine-sensitising factor;
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UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
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                                 94US-0292968.
93US-0110947.
94US-0251121.
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93US-0110947.
94US-0251121.
                                                                                   98US-0082514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolated pertussis holotoxin useful in studying functional resemblance -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                 SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 21;
Pred. No. 0.00045
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                 26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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(CONN-) CONNAUGHT LAB LTD

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Search completed: October 24, 2002, 15:35:02 Job time: 19.6885 secs
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                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promotting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin. Pertussis toxin is the cause of whooping cough following infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                    by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-122260/13.
                                                                        40 VEVPGSQHIDSQ 51
                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cockle SA,
Stein PE;
                                                                                                                                                                                                                   93 AA;
                                                                                                                                          100.0%;
nilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oomen RP,
                                                                                                                                            0;
                                                                                                                                            Score 62; DB 22; Length 93; Pred. No. 0.00045; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loosmore S,
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
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222222111654
2254321098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
         seq
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Match
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US-08-477-410-1
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US-09-313-215-14
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Sequence 71, Appl	Sequence 8, Appli	Sequence 193, App	Sequence 22, Appl	Sequence 30, Appl	Sequence 16, Appl	∵.	Sequence 29, Appl	Sequence 11, Appl	Sequence 5, Appli	Sequence 12, Appl	Sequence 13, Appl	•	Sequence 10, Appl	Sequence 9, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 24, Appl

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                                Matches
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Best Local Similarity
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
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APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 10
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Ontario
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Suite 701, 330 University Avenue
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                             100.0%; ilarity 100.0%; Conservative 0;
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OOMEN, Raymond P.
                                                                                                                                                                                             (416) 595-1163
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24-AUG-1993
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US-08-467-976-26
Sequence 26, Application US/08467976
Patent No. 6018022
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US-08-467-536-26
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                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24 AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
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APPLICATION NUMBER: US 08
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
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MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                      LENGTH: 93 amino acids TYPE: amino acid STRANDEDNESS: single
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M5G 1R7
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Suite 701, 330 University Avenue
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KLEIN, Michel H.
ARMSTRONG, Glen D.
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STEIN, Penelope E.
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                                                                                                                                                                                                                                                                                                                                                                                  1038-455 MIS:vg
                                                                                                                                                                           Score 62; DB 2;
Pred. No. 0.00032;
                                                                                                                                                              Mismatches
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                                                                                                                                                                                          Length 93;
                                                                                                                                                              Indels
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GENERAL INFORMATION:

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US-09-082-514-26
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                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                          GENERAL INFORMATION:
APPLICANT: READ, RAPPLICANT: STEIN, APPLICANT: COCKLE,
                                                                                                                                                              Patent No.
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                             Matches
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ZIP: M5G 1R/
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOTAL PC-DOS/MS-DOS
TOTAL PC-DOS/MS-DOS
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EILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
                              APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAE! I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
               APPLICANT: HAZES, Bart TITLE OF INVENTION: MOD
                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                            40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                             6, Application US/09082514 6168928
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                                                      READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                           Conservative
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                                          ARMSTRONG, Glen D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEIN, Penelope
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             MODIFICATION OF PERTUSSIS TOXIN
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46
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Pred. No. 0.00032;
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; ORGANISM: Homo sapiens
US-09-069-023-15
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TOPOLOGY:
US-09-082-514-26
                                                                                                                                                                        SOFTWARE: PatentIn
SEQ ID NO 15
LENGTH: 93
                                                              Matches
                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1:
Patent No.
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APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING LATER CHASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 0f
APPLICATION NUMBER: US 0f
APPLICATION NUMBER: 24-NGC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: ou.
CITY: Toronto
Omate: Ontario
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LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                              Local Similarity hes 5; Conserv
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Local Similarity 100.0%;
Local Similarity 00.0%;
Local 12; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/082,514 FILING DATE:
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2 MPGSQHV 8
                            3 VPGSQHI 9
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o. 6348573
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6th Floor, 330 University Avenue
                                                              Conservative
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linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                             Ver.
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                                                                            54.88;
71.48;
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                                                                              Score 34;
Pred. No.
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Pred. No. 0.00032;
); Mismatches 0;
                                                              Mismatches
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RESULT 8
5208144-18
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APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L.
TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA
CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-726-306A-101
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US-08-726-306A-101
               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/726,306A FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jun-1996
FILING DATE: 01-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101,
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/39
FILING DATE: 22-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 313,682
FILING DATE: 22-FEB-1989
APPLICATION NUMBER: 235,211
FILING DATE: 23-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 345-911
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
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NAME: Williams, Ph.D., Kathl
REGISTRATION NUMBER: 34,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
LENGTH: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM PC compatible
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                   NO:18:
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                                                                                                                                          US/07/396,697
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31;
Pred. No.
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US-08-477-108A-11
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/477,108A FILING DATE: June 7, 1995 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowicz, Anthony
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07,
FILING DATE: 09/01/92
APPLICATION NUMBER: 07,
FILING DATE: 02/28/92
APPLICATION NUMBER: 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                     TELLEFAX: (V-
TELEFAX: 200154
                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                    NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 0: FILING DATE: 09/01/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 IPGOWHCDRQ 32
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nes 5; Conserv
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1 IEVPGARILQHKD 13
                                                                                                                                                                      LENGTH:
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                          1 VEVPGS---QHID 10
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5801001
                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 Franklin Street
                                                                                                                                                                                                                             (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                       Conservative
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Pred. No.
                                                                    Score 30.5;
Pred. No. 18;
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RESULT

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Sequence 12, Application US/08747410 Patent No. 5993820

GENERAL INFORMATION:

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; ORIGINAL SOURCE:
US-08-747-410-12
                                                                                                                                                                                                                     PCT-US92-07813-26
                                                                                                                                                                                    Sequence 26, Application PC/TUS9207813 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REBERENCE/DOCKET NUMBER: 11526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE NY HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                      APPLICANT: LESNIEWSKI, RICHARD R. APPLICANT: LEUNG, TAT K. TITLE OF INVENTION: HEPATITIS C A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 12-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3100 No. 5
CITY: Minneapolis
                COUNTRY: U.S.A. ZIP: 60064-3500
                                                           CITY: ABBOTT PARK
                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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READABLE FORM:
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                                            ILLINOIS
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                                                                         ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                Conservative
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100.0%; Pred. No.
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US-09-003-708A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: WU, Jen
APPLICANT: CHEN, J
APPLICANT: CHANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 708-937-636
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKIP, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4767.P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Pro-
TITLE OF INVENTION: Act.
TITLE OF INVENTION: Pol.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07813
                                REFERENCE/DOCKET NUMBER: AC TELECOMMUNICATION INFORMATION: TELEPHONE: (202)-347-2600
                                                                                                     FILING DATE: January 10, ATTORNEY/AGENT INFORMATION: NAME: Ronald R. Snider
                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.5 inch, MEDIUM TYPE: storage COMPUTER: IBM PC compatible
                              TELEPHONE:
                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER: US/09/003,708A
FILING DATE: 01/07/98
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 27613
CITY: Washington, D.C.
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P.O. Box 27613
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CHANG, Chi-Yao
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y 10, 1997
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Pred. No.
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; HYPOTHETICAL: NO
US-09-003-708A-6
                              Matches
                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6235874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WU, Jen
APPLICANT: CHEN,
                                                                                                                                                                          TELEFAX: (202)-347-787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/
FILING DATE: 01/07/98
APPLICATION NUMBER: 60/
FILING DATE: January 10
                                                                                                  TOPOLOGY: Un
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ACA-001-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-347-2600
TELEPAX: (202)-347-7870
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Fei-Fei Chao
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/003/708
FILING DATE: January 10, 1997
APPLICATION NUMBER: 09/003/708
                           Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 EVPKKQHV 27
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les 5; Conservative
                                                                                                                                                               LENGTH:
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                                                                                                                                                amino acid
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                              Conservative
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CHEN, Jyh-Yih
                                                                                                                                  Unknown
                                                                                                                 polypeptide
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                                           48.4%;
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                                                                                                                                                                                                                                                                  43,538
                           : Score 30; DB
: Pred. No. 1.7e
1; Mismatches
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Pred. No.
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                       , DB 4; Lc..
, 1.7e+02;
, 2;
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1.7e+02;
2;
                                                     Length 98;
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; Sequence 125, Application US/09314268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/314,268
                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                            US-09-314-268-125
                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: US-08-934-915-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-934-915-14
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DILLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DILLNER,
APPLICANT: CHENG, HW
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LOUISE A. Foutch REGISTRATION NUMBER: 37,13 REFERENCE/DOCKET NUMBER: 19 TELECOMMUNICATION INFORMATION: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3.0 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 17/5/ U.S
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/934,915 FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EVPKKQHV 27
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5932412
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amino acid
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DILLNER, LENA
                                                                                                                                                                                                                                                                                                                                             Conservative
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,133
                                                                                                                                                                                                                                                                                                                                             Score 29; DB;
Pred. No. 45;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7654321	Result No.
55555555555555555555555555555555555555	Score
100.0 100.0 100.0 100.0 100.0	Query Match Length DB ID
12 15 15 21 21 93	ength D
5 5 2 1 1 1 2 1	₩.
US-09-786-648-3 US-08-732-371A-1 US-08-732-371A-1 US-09-786-648-4 US-09-786-648-5 US-08-110-947A-26	ID
Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 5, Appli Sequence 10, Appl Sequence 26, Appl	Description

9

1 VEVPGSQHIDSQ 12

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2225,	e 2176		3025,	1129,	1132	645,					4087,	1008	Sequence 448, App	Sequence 389, App	Sequence 2501, Ap	Sequence 6, Appli	Sequence 6, Appli	Sequence 583, App	Sequence 352, App	æ	N	5651, 1	2964	2967		16,	11193,	477,	917	6316,	488		18		470	e 2,	Sequence 26, Appl

ALIGNMENTS

Query Match 100.0%; Score 62; DB 21; Length 12; Best Local Similarity 100.0%; Pred. No. 0.00041; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gap	; LENGTH: 12; TYPE: PRT; ORGANISM: E. coli; FEATURE: ; FEATURE: 5061; LOCATION: 5061; OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivabl; OTHER INFORMATION: human variant E. coli US-09-786-648-3	RESULT 1 US-09-786-648-3 : Sequence 3, Application US/0978664B : General Information: : APPLICATT: Williams, Neil Andrew : APPLICATT: Williams, Neil Andrew : APPLICANT: Hirst, Timothy Raymond : TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci : TITLE OF INVENTION: Adjuvants : FILE REFERENCE: 7438 : CURRENT APPLICATION NUMBER: US/09/786,648 : CURRENT APPLICATION NUMBER: US/09/786,648 : CURRENT FILING DATE: 2001-03-07 : PRIOR APPLICATION NUMBER: PCT/GB99/02970 : PRIOR FILING DATE: 1999-09-07 : NUMBER OF SEQ ID NOS: 6 : SOFTWARE: MS DOS
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VEVPGSQHIDSQ 12

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US-08-732-371A-1
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US-08-732-371-1
                                                                Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/UB/12571
GENERAL INFORMATION:
APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: AGAING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                        Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 09-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                        ADDRESSEE:
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                            419 Seventh
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419 Seventh Street, N.W., Suite 300
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ilarity 100.0%;
Conservative 0
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                                          BROWDY AND NEIMARK
                           Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/732,371
                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                   Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                    0.00053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-786-648-4
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 12
                                                                                   Query Match
Best Local Similarity
                                                                    Matches
                                                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/GB99/02970 PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                       LOCATION: 45...65
OTHER INFORMATION: isolated or synthetic
OTHER INFORMATION: human variant E. coli
                                                                                                                                                                                                                      LENGTH: 21
TYPE: PRT
ORGANISM: E. coli
                                                                                                                                                                                                          FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPUTER: OF COMPUTER: FLOPOS/MS DOS
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-MAY-1994 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37,971 REFERENCE/DOCKET NUMBER: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: YUN, Allen C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 09-JAN
σ
                  1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-628-519
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VEVPGSQHIDSQ 12
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VEVPGSQHIDSQ 17
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12; Conserv
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                 ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version
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03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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09-JAN-1997
                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 11; 100.0%; Pred. No. 0.00053;
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                                                                                   Score 62; DB 21;
Pred. No. 0.00079;
                                                                    Mismatches
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                                                                                                                                                                       EtxB beta4-alpha2 loop fragment derivabl
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                                                                                                 Length 21;
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                                                                  0;
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                                                                  Gaps
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RESULT 5 US-09-786-648-5

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RESULT 6
US-08-110-947-10
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LENGTH: 21
TYPE: PRT
ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08110947 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
                               TELEFAX: (703) 415-081
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 45...65
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810 TELEFAX: (703) 415-0813
                                                                                                                                                                                  FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Shoemaker and Mattare, Ltd.
STREET: Suite 1203 Crystal Plaza I, 2001 Jefferson
STREET: Davis Hwy.
CITY: Arlingfon
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Vi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 12; Conserv
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                 NAME: FALLOW, Charles REGISTRATION NUMBER: 2
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/110,947 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 22202-0286
             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VEVPGSQHIDSQ 12
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: 93 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          READ, Randy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OOMEN, Raymond P
KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCKLE, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEIN, Penelope E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated or synthetic {\tt EtxB} beta4-alpha2 loop fragment derivable porcine E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                              28,946
                                                  10:
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Pred. No. 0.00079;
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US-08-110-947A-26
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                                                                                                                                                                                                                                                                                     US-08-110-947A-26
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                     Matches
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APPLICANT:
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RESULT 8

US-08-251-121-26

; Sequence 26, Application US/08251121

; GENERAL INFORMATION:

; APPLICANT: READ, Randy J.

; APPLICANT: STEIN, Penelope E.

APPLICANT: COCKLE, Stephen A.

; APPLICANT: COKELE, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08110947A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,947A
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATICAL CALLED IN AUGUST AND AUGUST AUGUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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STREET: Suite 1203 Crystal Plaza I, 2001 Jefferson
STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 415-0813 TELEX: 89-9456 LUKPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
les 12; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VEVPGSQHIDSQ 12
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STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEIN, Penelope E
COCKLE, Stephen A
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                                                                                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raymond P
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Pred. No. 0.0044;
Mismatches 0
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Pred. No. 0.0044;
; Mismatches 0;
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KLEIN, Michel H. ARMSTRONG, Glen D.

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RESULT 9
US-09-786-648-2
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                                                                                                             SOFTWARE: MS DOS
SEQ ID NO 2
LENGTH: 7
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/251,121
FILING DATE: 31-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine TITLE OF INVENTION: Adjuvants FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
OTHER INFORMATION: OTHER INFORMATION:
                                                       FEATURE:
                                                                         ORGANISM: E.
                                     LOCATION: 51...57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VEVPGSQHIDSQ 12
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Suite 701, 330 University Avenue
                                                                           coli
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isolated or synthetic {\tt EtxB} beta4-alpha2 loop fragment derivable human variant {\tt E.} coli
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Pred. No. 0.0044;
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Sequence 4/0, ALEJANDROV, Nickolai APPLICANT: ALEXANDROV, Nickolai APPLICANT: BROVER, Vyacheslav TITLE OF INVENTION: Sequence-D TITLE OF INVENTION: Thereby TITLE OF THE APPLICANT: US/
                                                   ; ORGANISM: Homo sapiens US-09-866-066-35
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Best Local Similarity
"~+~hes 6; Conserve
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: OTHER INFORMATION: Ceres Seq. ID no. 1024399
: NAME/KEY: misc_feature
: LOCATION: ()..()
: OTHER INFORMATION: Xaa is any aa, unknown or other US-09-595-298A-470
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Best Local Similarity
'`~+ hes 7; Conserva
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                                                                                                ; NUMBER OF SEQ I
; SOFTWARE: Paten
; SEQ ID NO 35
; LENGTH: 51
Query Match
Best Local Similarity
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                                                                                                                                                   PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/207,257 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: 60/207,152 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/866,066
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                       APPLICANT: Karnovsky, Alla TITLE OF INVENTION: Human Ion Channels FILE REFERENCE: 00229.US1
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Benjamin, Christopher
APPLICANT: Roberds, Steve
APPLICANT: Ruble, Cara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/595,298A CURRENT FILING DATE: 2000-06-16
                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/207,119
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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TYPE: PRT
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NAME/KEY: peptide
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                                                                                                                                     PatentIn
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Gotow, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09866066
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50.0%;
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 Score 36;
Pred. No.
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Pred. No.
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Pred. No.
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 DB 22;
1.2e+02;
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                 Length 51;
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RESULT 14
US-08-827-356-4889
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US-09-465-854-18
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US-09-465-854-18
                                                               Sequence 4889, Application US/08827356 GENERAL INFORMATION:
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SEQ ID NO 18
LENGTH: 75
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Best Local 9
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                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kinney, Anthony J.
APPLICANT: Lane, Tanmy M.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Plant burine Biosynthetic Genes
FILE REFERENCE: BB-1323-Pl
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/112,736
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 8
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CURRENT FILLING DATE: 1999-12-17
EARLIER APPLICATION NUMBER: 60/112,736
EARLIER FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kinney, Tony M.
APPLICANT: Lane, Tammy M.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Purine Biosynthetic Genes
FILE REFERENCE: BB1323 US NA
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word 7.0A
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                               APPLICANT:
   APPLICANT:
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                                                                                                                                                                                                                       6; Conserv
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George H. Shimer, Jr.
George H. Miller
Roberta S. Hare
Karen J. Shaw
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75.0%;
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75.0%;
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; Pred. No. 2.8e
1; Mismatches
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1; Mismatches
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2.8e+02;
hes 1;
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                             APPLICATION NUMBER: US 09/266,555
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR FILING DATE: 1999-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                     Sequence 6316, Application US/09611529 GENERAL INFORMATION:
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              PRIOR APPLICATION NUMBER: US
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INFORMATION FOR SEQ ID NO: 4889:
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                                                                                                                                                                                                                                                                                                       APPLICANT:
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LENGTH: 91 amino acids
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FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,477
FILING DATE: 01-APR-1996
PRILING DATE: 01-APR-1996
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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ZIP: 07033-0530
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                                                                                                                                                                                                                                                                                      George H. Shimer, Jr.
George H. Miller
Roberta S. Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Schering-Plough Corporation
2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAPHYLOCOCCUS AUREUS RELATED COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%;
36.4%;
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Pred. No.
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Gaps

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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length: 100
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Match
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1. /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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137.008 Million cell updates/sec
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62
1 VEVPGSQHIDSQ
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Copyright (c) 1993 - 2002 Compugen
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                                      US-10-105-299-5379
US-10-182-998-14649
US-10-203-138-15-288
US-10-203-138-15-288
US-10-203-139-30215
US-10-182-995-23617
US-10-203-134-29975
US-10-182-993-29973
US-10-182-997-22308
US-10-182-998-13801
US-10-182-998-13801
US-10-203-137-30270
US-10-203-138-14266
US-10-106-698-6662
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US-09-547-599C-2428
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US-09-513-996A-3966
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US-10-106-698-6673
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9470, Ap
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US-10-040-862-1215	US-10-235-954-752	US-08-905-054B-26	US-10-217-607-1183	US-10-203-139-37109	US-10-182-993-37688	US-09-684-197A-5	PCT-US02-09921-833	US-09-791-537-111453	US-10-203-139-30553	US-10-203-137-31597	US-10-203-135-30509	US-10-182-997-23638	US-10-182-993-30655	US-10-203-136-31414	US-10-203-134-31357	US-10-182-995-24943	US-10-212-778-1146	US-10-212-759-1554
Sequence 1	Sequence 7	Sequence 2	Sequence 1	Sequence 3	Sequence 3	Sequence 5	Sequence 8	Sequence 1	Sequence 3	Sequence 3	Sequence 3	Sequence 2	Sequence 3	Sequence 3	Sequence 3	Sequence 2	Sequence 1	Sequence 1
1215, Ap	752, App	26, Appl	1183, Ap	37109, A	37688, A	, Appli	833, App	111453,	30553, A	31597, A	30509, A	23638, A	30655, A	31414, A	31357, A	24943, A	1146, Ap	•

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; TYPE: PRT; CRGANISM: Zea mays; US-10-155-881-12211
CURRENT APPLICATION NUMBER: US/09/547,599C
CURRENT FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 08/905,223
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
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US-10-155-881-12211
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
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SEQ ID NO 12211
LENGTH: 87
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Best Local Similarity 41.7
Matches 5; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Lutflyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                     APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: Expressed Sequence Tags
FILE REFERENCE: GEN-T119C1
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41.7%;
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US-09-540-209B-9470
; Sequence 9470, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: GATY L. Breton
; APPLICANT: GATY L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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US-10-143-775-583
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                                                                                                                 RESULT 4
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SEQ ID NO 583
LENGTH: 96
TYPE: PRT
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LENGTH: 93
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CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PCO21C1N
FILE
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PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,133
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
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SOFTWARE: Patent.pm
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PRIOR FILING DATE: 1997-08-01
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REFERENCE:
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score 7.00
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Pred. No.
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.3e+02;
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                                                                                                                                                                                                                                                                  Length 96;
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; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-9470
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                                                                                                                                                                                   Sequence 3025, Appli GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 645, Application US/10217648 GENERAL INFORMATION:
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Matches 6; Conserv
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SEQ ID NO 9470
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                                                                                                                                   APPLICANT:
                                                                 APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 09/758,440
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
APPLICANT: HOWARD M. Grey
APPLICANT: ROBERT Chesnut
TITLE OF INVENTION: INDUCTING CELLULAR IMMUNE RESPONSES
TITLE OF INVENTION: HEPATITIS B VIRUS USING PEPTIDE AN
                                                                                                    APPLICANT:
                                                                                                                     APPLICANT:
                                                                                                                                                                    APPLICANT: Alessandro Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PM015C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (64)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                      31 DLPGARHDDPQ 41
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                                                                                                                                                                                                                                                                                                                                                    l Similarity
5; Conserv
                                                                                                Maria A. Vitiello
Brian D. Livingston
                                                                                                                                   Scott Southwood
                                                                                                                                                    John Sidney
                                                                 Esteban Celis
Ralph T. Kubo
                                                                                                                                                                                                     Application US/09350401A
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45.5%;
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Pred. No.
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   AND
   NUCLEIC ACID
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US-09-350-401A-3025
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                                                                          SEQ ID NO 3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-350-401A-3183
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/350,401A
CURRENT FILING DATE: 1990-07-08
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
                                                                                        PRIOR FILING DATE: 1993-07-04
NUMBER OF SEQ ID NOS: 3877
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INDUCING CELLULAR IMMUNE TITLE OF INVENTION: HEBATITIS B VIRUS USING TITLE OF INVENTION: COMPOSITIONS FILE REFERENCE: 2060.0060008
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CURRENT FILING DATE: 1999-07-08
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                                   LENGTH: 15
TYPE: PRT
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence FEATURE:
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OR FILING DATE: 1998-11-10
OR APPLICATION NUMBER: US 08/205,713
OR FILING DATE: 1994-03-04
OR APPLICATION NUMBER: US 08/159,184
OR FILING DATE: 1993-11-29
OR APPLICATION NUMBER: US 08/073,205
OR APPLICATION NUMBER: US 08/073,205
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APPLICATION NUMBER: US 60/013,363
FILING DATE: 1996-03-13
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/189,702 FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/013,363 FILING DATE: 1996-03-13
                                                                                                                                             APPLICATION NUMBER: US 08/159,184 FILING DATE: 1993-11-29 APPLICATION NUMBER: US 08/073,205
                                                                                                                                                                                                      APPLICATION NUMBER: US 08/205,713 FILING DATE: 1994-03-04
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Robert Chesnut
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Brian D. Livingsto
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Ralph T. Kubo
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Pred. No.
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RESULT 8
US-10-106-698-6673
; Sequence 6673, Appli
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                   US-10-235-953-3603
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen et
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserv
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OTHER INFORMATION: Xaa equals an NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals at NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 3.0 SEQ ID NO 6673
                                CURRENT APPLICATION NUMBER: US/10/235,953
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 09/758,471
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PH002CIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR TILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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CURRENT FILING DATE: 2002-03-27
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PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (8)
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OTHER INFORMATION:
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Pred. No.
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Pred. No. 1.8e+02;
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US-09-513-996A-3966
US-09-513-996A-3966
Sequence 3966, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
; ORGANISM: Homo US-10-105-299-5379
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US-10-105-299-5379
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                                                                                                                                                                Sequence 5379, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
                                                                Prior Application removed - SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 5379
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 41.7
Matches 5; Conservative
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SEQ ID NO 3966
LENGTH: 89
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                                                                                                               CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCODED THEREBY FILE REFERENCE: 2750-709P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/513,996A CURRENT FILING DATE: 2000-02-25
                               LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: UNSURE
LOCATION: 1..89 /
OTHER INFORMATION: any n or Xaa = unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Location 1..89 / Ceres Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                     1 VEVPGSOHIDSQ 12
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                                                                                                                                                                                                                                                                                                                      VETPGCVHVKTE 41
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             sapiens
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41.7%;
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                                                                                                 See File Wrapper or Palm
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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2.2e+02;
5;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 89;
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                                                                                                                                               US-10-203-135-30068
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Best Local Similarity
Watches 5; Conserv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PRIOR DATE: 04 February 2000 (04.02.00)
PRIOR PRIOR PATEION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 28 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PRIOR PRIOR DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PRIOR DATE: 03 OCTOBER 2000 (03.10.00)
PRIOR PRIOR DATE: 03 COCTOBER 2000 (27.09.00)
PRIOR FILING DATE: 27 September 2000 (27.09.00)
                                                                                                              Sequence 30068, Appl GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Molecular Dynamics SEQ ID NO 14849
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HBL 100
FILE REFERENCE: PB 0004 WO 9
                                      APPLICANT:
                                                             APPLICANT:
                                                                            APPLICANT:
                                                                                           APPLICANT: Molecular Dynamics,
                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/234,687
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OTHER INFORMATION:
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CANT: Hanzel, David K. CANT: Chen, Wensheng OF INVENTION: HUMAN GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21 September 2000 (21.09.00) APPLICATION NUMBER: US 09/608,408
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                                                         Penn, Sharron
Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn, Sharron
Rank, David R
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                                                                                                                                Application US/10203135
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71.4%;
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   GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
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Pred. No. 1.9e
3; Mismatches
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Pred. No.
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1.9e+02;
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OF INVENTION:

ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG

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US-10-203-138-15288
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                                                                                                                                                                         PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 40/632,366
PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/203,138
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 W0 8
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CURRENT FILING DATE: 2002-08-02
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TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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OTHER INFORMATION:
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APPLICATION NUMBER: US 60/216,359
FILING DATE: 27 September 2000 (27.09.00)
APPLICATION NUMBER: US 60/214,687
FILING DATE: 21 September 2000 (21.09.00)
APPLICATION NUMBER: US 09/668,408
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FILING DATE: 26 May 2000 (26.05.00)
APPLICATION NUMBER: US 09/632,366
FILING DATE: 03 August 2000 (03.08.00)
APPLICATION NUMBER: GB 24263.6
FILING DATE: 03 October 2000 (03.10.00)
                                                                                                 APPLICATION NUMBER: US 09/608,408 FILING DATE: 30 Through 100 Processing Control of the Control 
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                                                          ID NOS:
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Pred. No. 2;
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                                                                          ; OTHER INFORMATION: US-10-203-139-30215
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR PPLICATION NUMBER: US 60/207,466
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR PPLICATION NUMBER: 03 0ctober 2000 (03.10.00)
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: 27 September 2000 (27.09.00)
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US-10-203-139-30215
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     Best Loc
Matches
                                       Query Match
                                                                                                                                                                                                                                                                                            SEQ ID NO 30215
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                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/203,139
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
FILE REFERENCE: PB 0004 WO 4
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ
SOFTWARE: MOLE
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
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Rank, David R
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ID NOS: 37156
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R.Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Accession: H95167
A; Status: preliminary
A; Status: preliminary
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95152
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-79 < KUPS;
A; Cross-references: GB: AEC05672; PIDN: AAK75537.1;
A; Experimental source: strain TIGR4
C; Genetics:
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A; Gene:
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C;Date: 03-Aug-2001 #sequence_revision
C;Accession: C95152
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A; Residues: 1-79 < KUR>
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39;
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                                                             PID:g14972931; GSPDB:GN00164;
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Radune, D.; Holtzappl
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TIGR:

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RESULT 5
T24159
 hypothetical protein R11.4 - Caenorhabditis elegans c;Speckes: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 ic;Accession: T24159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA2021 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G83393 R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicke adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbi; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                           R; Figueroa-Bossi, N.; Bossi
submitted to the EMBL Data
A; Reference number: Z14818
A; Accession: T02997
                                                                                                                                                                                                                                                                                                                                                                                                               sigma-E factor regulatory protein rseA - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-199
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A;Residues: 1-74 <STO>
A;Cross-references: GB:AE004628; GB:AE004091; NID:g9948018; PIDN:AAG05409.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A; Residues: 1-35 <FIG>
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A; Accession: G83393
A; Status: preliminary
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nes 6; Conserv
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ce: strain LT2
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50; MUID:20437337
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Pred. No. 70;
3; Mismatches
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A.; Larbig,
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A; Molecule type: mRNA
A; Residues: 1-31 <KUM>
C; Superfamily: GTP-bin
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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.
A;Title: Genome of the Bacterium Streptococcus pneumoniae
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98034
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c;Date: 22-Oct-2001 #sequence_revisi
C;Accession: B98034
R;Hoskins_J.A.; Alborn Jr., W.; Arr
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Submitted to the EMBL Data Library, November
A; Reference number: Z19847
A; Accession: T24159
A; Status: preliminary; translated from GB/EME
                                                                                                                         A; Title: Regulation and function of G-alpha A; Reference number: A32384; MUID:89195237 A; Accession: A32384
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C;Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #text_change 19-Jul-1996
                                                                                                                                                                                                                                                       G-alpha-1 protein - slime mold (Dictyostelium sp.) (fragment)
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A; Map position: X
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A; Residues: 1-65 <WIL>
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ce: clone R11
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J.; Matsushima,
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                                                                                                             not compared with conceptual
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                                                                                                                                                                                           Devreotes, P.N.; Firtel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Baltz, R.H.; Jaskunas,
Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                             Dictyostelium
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EVPGSQHIDS

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RESULT 9

117876
hypothetical protein a376R - Chlorella virus PBCV-1
c;Species: Chlorella virus PBCV-1
c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17876
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                               RESULT 10
E71527
E71527
hypothetical protein CT330 - Chlamydia trachomatis (serotype D, : C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change (C;Date: 13-Sep-1998)
C;Accession: E71527
C;Accession: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genet:
A; Note:
                                                                                                                                                           R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen A; Reference number: A71570; MUID:99000809
A; Accession: E71527
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A; Residues: 1-70 <RES>
A; Cross-references: EMBL: U281:
A; Note: chromosome 15-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Disruption of the architectural factor A; Reference number: I39058; MUID:95330810 A; Accession: I39058
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Cell 82, 57-65, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #text_change 05-Nov-1999
                                A; Molecule type: DNA
A; Residues: 1-90 <ARN>
A; Cross-references: GB
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A; Accession: T17876
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         A; Experimental source:
                                                                                                                                A; Status: preliminary
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A; Residues: 1-84 <GRA>
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Best Local
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GB:AE001306; GB:AE001273; NID:g3328748; ce: serotype D, strain UW-3/Cx
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be: specific h
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71.48;
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host Chlorella
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Pred. No. 1.6e+02;
1; Mismatches 1
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Pred. No.
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1.3e+02;
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                                    PIDN: AAC67925.1;
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breakpoint
                                                                                                                                                                                                                                                                                        R.; Aravind, L.; Mitchell
                                                                                                                                                                                                                         of humans: Chlamydia trac
                                                                                                                                                                                                                                                                                                                                                                                                                  strain UW3/Cx)
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RESULT 11
S06461
hypothetical protein nifD2 region - Ana
C:Species: Anabaena variabilis
C;Date: 05-Mar-1999 #sequence_revision
                                                RESULT
S70252
                                                                                                                                                                                                                                                                                                                                                                       myelin basic protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Oct-1992 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dyst C; Keywords: alternative splicing F; 6-98/Domain: alpha-actinin actin-binding domain homology (fragment) <AAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Duchenne muscular dystrophy gene product is not identical in muscle and A;Reference number: $506461; MUID:$9082658 A;Accession: $506461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 10-Oct-1997
C;Accession: S06461
R;Nudel, U.; Zuk, D.; Einat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe. D
                                                                                                            В
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                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-33 < ARU
                                                                                                                                                                                                                                                             A; Reference number: A60222;
A; Accession: A60222
A; Status: preliminary
                                                                                                                                                                                                                                                                                               A;Title: Identification of the new isoforms A;Reference number: A60222; MUID:91162193
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J. Neurochem. 56, 1222-1226, 1991
                                                                                                                                                                                                                                                                                                                                                         C; Accession: A60222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the list of introns may be incomplete
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A; Residues: 1-98 < NUD>
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A;Gene: CT330
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Best Local S
Matches 4
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5; Conserv
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50.0%;
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71.48;
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Pred. No.
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Pred. No.
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                              Anabaena variabilis (fragment)
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No.
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1.8e+02;
1;
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1.7e+02;
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87;
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05-Mar-1999

#text_change 05-Mar-1999

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R.Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A;Reference number: A97359; PMID:11743194

A;Accession: D98143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-52 <SCHA
A,Residues: 1-52 <SCHA
A,Cross-references: EMBL:U25172; NID:1160349
A,Experimental source: ATCC 29413
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A,Note: This is the hypothetical translation of a sequence translated in an incorrect
                                                                                                                                                                                                                                                                                    hypothetical protein AGR_L_207 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: D98143
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
D98143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetolactate synthase (EC 4.1.3.18) III large chain - Salmonella typhimurium C;Species: Salmonella typhimurium A;Variety: strain LT2 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 15-Oct-1999 C;Accession: S15939; S14545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S70252
R;Schrautemeier, B.; Neveling, U.; Schmitz, S.
Mol. Microbiol. 18, 357-369, 1995
A;Title: Distinct and differently regulated Mo-dependent nitrogen-fixing systems evolved egions as part of the nifl/2 gene clusters.
A;Reference number: S70242; MUID:96296457
A;Accession: S70252
                                           A; Molecule type: DNA
A; Residues: 1-72 <KUR>
A; Cross-references: GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: ilv'I
C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Jahreis, K.; Postma, P.W.; Lengeler, J.W.
Mol. Gen. Genet. 226, 332-336, 1991
A;Title: Nucleotide sequence of the ilvH-fruR gene region of Escherichia coli K12 and A;Reference number: S15939; MUID:91238714
A;Accession: S15939
A;Molecule type: DNA
A;Residues: 1-59 <JAH>
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A; Gene: AGR_L_207
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C;Genetics:
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                                           GB:AE007870; PIDN:AAK88670.1; PID:g15158399; GSPDB:GN00170
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A; Map position:

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Best Local S
Matches 4
64 PGSSHVN 70
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                                        Similarity
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Pred. No.
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Search completed: October 24, 2002, 15:37:43 Job time: 11.0492 secs

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Gapop 10.0 , Gapext 0.
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62
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    FER_MASLA
RS13_THETH
Y13F_BPT4
Y13F_BPT4
PP12_PERAM
PH2_PERAM
PH3_PERAM
IMB_MOUSE
CSPA_BACCE
UBIQ_DICOL
TAT_HYLMA
Z600_DROME
APC2_MOUSE
RL23_MYCLE
YABP_BACSU
DNAJ_STRAL
LCRS_YERPE
EM6_ARATH
RL25_ECOLL
DNAJ_STRAL
LCRS_YERPE
EM6_RATH
RL25_ECOLL
PERZ_CYACA
PERZ_NOSMU
FER_NOSMU
FER_NOSMU
FER_PIPBB
FERZ_PIPBB
FERZ_PIPBB
FERZ_PIPBB
FERZ_MYCHO
RL23_MYCHO
RL23_MYCHO
RL23_MYCHO
RL23_MYCHO
RL23_MSYCHO
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P82695 periplaneta
P82696 periplaneta
Q9qut4 mus musculu
Q45096 bacillus ce
P08618 dictyosteli
P04613 human immun
P22469 drosophila
Q05020 mus musculu
Q3298 mycobacteri
P37578 bacillus su
P31297 chinchilla
P14601 rhodobacter
P96457 streptomyce
Q00931 yersinia pe
Q02973 arabidopsis
P02426 escherichia
P15789 cyanidium c
P0543 anabaena sp
P00249 nostoc musc
P15788 synechococc
Q51577 plectonema
Q57401 yersinia en
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P80377 thermus agu
P39499 bacteriopha
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FER_MASLA
ID FER_M
AC P0024
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DE Ferre
GN PETF.
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ייייי בדפליובייי ל		_	P17728 leiurus qui				P45697 mesobuthus				Q48464 klebsiella	

ALIGNMENTS

Query Match Best Local Similarity Matches 5; Conser	HSSP; P06 InterPro; InterPro; InterPro; Pfam; PF0 PRINTS; PF0 PROSITE; Electron INIT_MET METAL METAL METAL METAL METAL METAL SEQUENCE		[1] SEQUENTER STR. "MO. "MO. "MO. "MO. "MO. "MO. "MO. "MO	OS Mastigocladus laminosus OC Bacteria; Cyanobacteria; OX NCBI_TaxID=1191;
46.8%; Score 29; DB 1; Length 98 larity 55.6%; Pred. No. 1e+02; Conservative 2; Mismatches 2; Indels	05543; 1CZP. 27 IPR000564; 2Fe2S_ferredoxin. 28 IPR0010541; Ferredoxin. 29 10111; fer2; 1. 29 10112; fer2; 1. 20 10113; fer2; 1. 20 10114; Ferredoxin. 20 10115; 2FE2S_FERREDOXIN; 1. 20 11 transport; Iron-sulfur. 21 10 10 21 1 IRON-SULFUR (2FE-2S) (BY 10 1 1 IRON-SULFUR (2FE-2S) (BY 10	pyright. e of Bio Institu utions an is not agreemee	P.R., Nechushtai R.; pof the petf gene encoding ferredox; bacterium Mastigocladus laminosus.", egister PGR98-027. sgister PGR98-027. shi S., Matsubara H., Rao K.K., Hall , Zuber H.; 78) to the PIR data bank. REDOXINS ARE IRON-SULFUR PROTEINS THE A WIDE VARIETY OF METABOLIC REACTIONS DS 1 2FE-2S CLUSTER.	laminosus (Fischerella sp.). obacteria; Stigonematales; Fischerella. 11;
98; els 0; Gaps 0;	SIMILARITY). SIMILARITY). SIMILARITY). SIMILARITY).	It is produced through a collaboration informatics and the EMBL outstation te. There are no restrictions on its long as its content is in no way removed. Usage by and for commercial nt (See http://www.isb-sib.ch/announce/.ch).	D.O.,	

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VEVPGSQHI

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RESULT 2

RS13_T
ID RS13_T
AC P80377
DT 01-FEB
DT 10-FEB
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Y13F_BPT4
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Hypothetical 10.1 k
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                 Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G. Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; "Bacteriophage T4 genome analysis."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Viruses; dsDNA vi
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01-FEB-1995 (Rel.
01-NOV-1995 (Rel.
                                              or send an
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical Y13F OR CD.3.
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Bacteria; Thermus/Deinococcus group; Thermus
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1. PE00416; RIBOSOMAL_S13; PARTIAL.

SITE; PS00646; RIBOSOMAL_S13; PARTIAL.
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  AF158101;
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4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                dsDNA viruses,
                                                                  requires a
                                         equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45586; PubMed=7957245; Herfurth E., Choli T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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AAD42549
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31,
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, Last annotation on
n S13 (Fragment)
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Last annotation update)
protein in cd-pseT intergenic region
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                                                                agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB
Pred. No. 33;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337F88EA0294D2A8
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DT 16-0C
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OC Blatt
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PH3_PERAM
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                      Query Match
                                                                                                                                                                                                                                          P82696;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Peptide hormone 3 (Pea-VEAacid 1).
                                                                                          Ann.
                                                                                                     of insects."
                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY OF TISSUE-Abdominal perisympathetic omeDLINE-20140865; PubMed-10676456; Predel R., Eckert M., Holman G.M.;
                                                                                                                                                                                             Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopterodea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: UNKNOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P82695;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peptide hormone 2 (Pea-VEAacid 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 91 AA; 10131 MW;
                                              Neuropeptide.
SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide.
SEQUENCE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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                                                                                                                                                                                   NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predel R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Abdominal
                                                                                                                 "The unique neuropeptide
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mes 6; Conser
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                                                                     MASS
                                                                   FUNCTION: UNKNOWN.
MASS SPECTROMETRY:
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l Similarity
6; Conserv
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5; Conserv
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           44.48;
75.08;
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75.08;
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                                              WW;
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 Score 27.5; t
Pred. No. 28;
1; Mismatches
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Pred. No. 1.5e
0; Mismatches
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Pred. No. 2
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01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
Major cold shock pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                 CSPA
                                                                                                                                                                                                                                                                                         CSPA_BACCE
Q45096;
                                                                                                                                                                                                                                                                                                                                         BACCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bauer M.F., Brunner M., Hofmann S.;
"Cloning and mapping of TimlO/DDP gene family encoding smiflinger proteins involved in mitochondrial carrier import."
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Mitochondrial inner membrane (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-Mouse, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitochondrial import inner membrane translocase subunit TIM8
(Deafness dystonia protein 2 homolog).
TIMMBB OR TIMBB OR DDP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
SEQUENCE FROM N.A.,
STRAIN-WSBC 10201;
MEDLINE-96213034; P
                                                                                     Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QUT4;
16-OCT-2001
                                                                                                                                                        Bacillus cereus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iransport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO04217; zf-Tim10_DDP.
Pfam; PF02953; zf-Tim10_DDP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1353424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                          36,28
                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
    PubMed=8631682;
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                                              AND SEQUENCE
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                                                                                                       Bacillus/Clostridium us group; Bacillus.
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; Translocation; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27.5;
Pred. No. 1
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                                              OF 1-28
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MBL outstation -
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RP SEQUEN
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01-AUG-1988 (Rel. C
01-AUG-1988 (Rel. C
01-NOV-1991 (Rel. C
                                                                                     Ohmachi T., Giorda R., Shaw D.R., Ennis H.I "Molecular organization of developmentally discoldeum ubiquitin cDNAs."; Biochemistry 28:5226-5231(1989).
                                                                                                                                                                                                                                                                                     terminal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88152253; PubMed-2831095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0050; CÓLDSHOCK.

PRODOM; PD000621; COLd_Shock; 1.

SMART; SM0357; CSE; 1.

PROSITE; PS00352; COLD_SHOCK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shock protein homologs from the ps 10201.";
J. Bacteriol. 178:2916-2925(1996).
-i- FUNCTION: CAN BIND TO ATTGG AN
                        SEQUENCE FROM N.A. MEDLINE-87257921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Activator; Multigene family. DOMAIN 5 64 CSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X93039; CAA63607.1; -. HSSP; P41016; 1C90.
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                                                                                                                                                                                        MEDLINE=89352609;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Mueller-Taubenberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Mycetozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold)
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-!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOWAIN (CSD) FAMILY.
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                                                                                                                                                                                                                                                                                                                                 "Complete cDNA
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"Identification and
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4; Conserv
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       Ennis H.L.
                                                                                                                                                                                                                                                             229:273-278(1988).
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                                                                                                                                                                                      PubMed=2548604;
                                                                                                                                                                                                                                                                                                           quence of a Dictyostelium ubiquitin with a carboxy-
identification of the protein using an anti-peptid
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Pred. No. 1.6e
2; Mismatches
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es 3;
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CRC64;
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                                                                                                                                                                                                                                                                                                           using an anti-peptide
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InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
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                                                                                                                                                 SEQUENCE
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Mol. Cell. Biol. 7:2097-2103(1987).
[4]
                                                                                                                                                                                                                          Nuclear protein; Polyprotein.
SITE 48 48
                                                                                                                                                                                                                                                           PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
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STRAIN-AX2;
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15
                                   \vdash
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FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEZINS, THE MALNTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
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D34080;
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LEVEGSDNIEN
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A34080.
B34080.
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AAA33264.1;
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AAA33266.1;
AAA33268.1;
CAA28408.1;
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AAA33261.1;
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AAA33262.1;
AAA33263.1;
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Pred.
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CONJUGATION TO ACCEPTOR PROTEINS
K -> N (IN SOME CLONES REPEATS).
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SYNTHESIZED AS A POLYUBIQUITIN
O TAIL REPEATS. SOME UBIQUITIN GENES
                                                                      Mismatches
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No.
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1.9e+02;
2;
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P04613;
13-AUG-1987
13-AUG-1987
16-OCT-2001
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P22469; Q9VUP1;
01-AUG-1991 (Rel. 19, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                        "Overlapping genes of Drosophila melanogaster: organization of the z600-gonadal-Eip28/29 gene cluster."; Genes Dev. 3:232-242(1989).
                                                                                              SEQUENCE FROM N.A. MEDLINE=89232719; Puschulz R.A., Butler
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                          Protein Z600.
Z600 OR CG17962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (MAL isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID-11697;
    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X04415; CAA28015.1; --
HIV; K03456; TAT$MAL.
InterPro; IPR001831; HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS I
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of two isolates from African patients. Cell 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.; "Genetic variability of the AIDS virus: nucleotide sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-86245056; PubMed-2424612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVPGSQH
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(Rel. 40, Last annotation
(Transactivating regulator
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RESULT 11
APC2_MOUSE
ID APC2_M
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heimann T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heimann T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krawitz S., Kulp D., Lal Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krawitz S., Kulp D., Lal Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McHalov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yle J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
C. --- PROTION: NOT KNOWN.
C. -- TEVENTION MENTAL STRAGE. TEVENDERITY DESTRIPTION FOR FABRY C.-
C. -- TEVENTION MENTAL STRAGE. TEVENDERITY DESTRETED TO FABRY
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A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hardon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hardon R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferrac C., Ferrac C., Ferson K.,
RA ROSler C., Gabra N.E., Garo N.S., Gelbart W.M., Classer K.
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Best Local S
Matches 5
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between
APC2_MOUSE STANDARD;
Q05020;
Q1-FEB-1994 (Rel. 28, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X58286; CAA41222.1; -
EMBL; AE003530; AAF49634.1;
PIR; A30172; A30172.
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       10530 MW;
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62.5%;
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19054C5965EE9109 CRC64;
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Smith H.O.,
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SEQUENCE
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BINDING
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032983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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MEDLINE-93162679; I
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Frants R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/RIJ;
MEDLINE=94010908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoffer M.J.V., Hofker Frants R.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and expression of the mouse apolipoprotein C2 Genomics 17:45-51(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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TISSUE SPECIFICITY: Secreted in plasma.
SIMILARITY: BELONGS TO THE APOC2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: APOC-II IS A COMPONENT OF THE VERY LOW DENSITY LIPOPROTEIN (VLDL) FRACTION IN PLASMA, AND IS AN ACTIVATOR OF SEVERAL TRIACYLIGLYCEROL LIPASES. THE ASSOCIATION OF APOC-II WITH PLASMA CHYLOMICRONS, VLDL, AND HDL IS REVERSIBLE, A FUNCTION OF THE SECRETION AND CATABOLISM OF TRIGLYCERIDE-RICH LIPOPROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
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Z22216; CAA80220.1; -.
Z22217; CAA80220.1; JOINED.
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PubMed=7916738;
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10741 MW;
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STRAIN-16051385; PubMed-7584024; MEDLINE-96051385; PubMed-7584024; Ogasawara N., Nakai S., Yoshikawa H.; Osasawara N., Nakai S., the 180 kilobase region of the Bacillus "Systematic sequencing of the 180 kilobase region of the Bacillus "Systematic sequencing the replication origin.";
                                                                                                                                                                                                                                                      YABP_BACSU
P37558;
                                                                                                                                                                                                                                                                                     BACSU
                                                                                                                   Bacteria; Firmicutes; B
Bacillus/Staphylococcus
NCBI_TaxID-1423;
                                                                                                                                                                                  YABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIBOSOMAI protein; rRNA-binding; Complete proteome. SEQUENCE 100 AA; 10939 MW; 1A9254F7D639DIAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00276; Ribosomal_L23; 1.
ProDom; PD001141; Ribosomal_L23;
PROSITE; PS00050; RIBOSOMAL_L23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                          01-OCT-1994
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- FUNCTION: BINDS TO A SPECIFIC REGION ON TH
                                                                                           SEQUENCE
                                                                                                                                                                 Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001014; Ribosomal_L23.
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OR ML1861 OR MLCB2492.04.
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protein in MFD-DIVIC in
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PUFQ_RHOCA
ID PUFQ_RHOCA
AC P14601;
DT 01-APR-1990
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GLUC_CHIBR
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P31297;
01-JUL-1993
01-JUL-1993
01-JUL-1993
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Chinchilla brevicaudata (Chinchilla)
Chinchilla brevicaudata; Crania
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Rodentia; Hystri
                                                                                                                                                                                                                                                                                                                       chemical assay.";
Peptides 11:683-685(1990)
-i- FUNCTION: PROMOTES ....
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                                                                                                                                                                                                         Pfam; PF00123; hormone2; 1
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCA; 1.
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EMBL; Z99104;
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-!- SIMILARITY: BELONGS
PIR; A60413; GCCB.
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                                                                                                                                                                                                                                                      ISSP; P01274; 1GCN
                                                                                                                                                                                                                                                                                                                                                         Eng J., Kleinman W.A., Chu L.S.;
"Purification of peptide hormones from chinchilla
                                                                                                                                                                                                                                           nterPro; IPR000532; Glucagon
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                                                                                                                                     Local
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INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS
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                                                                                                                          4; Conserv
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3; Conser
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100 AA; 1
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                      STANDARD;
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 14, Created)
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26, Last sequence up
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57.1%;
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1403 MW; OA3DFD6A75E8FF79 CRC64;
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98;
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Matches 4
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EMBL; M22752; AAA26168.1; -.
EMBL; 211165; CAA77551.1; -.
PIR; A28143; A28143.
PIR; A32253; A32253.
Photosynthesis; Chlorophyll biosynthesis.
Photosynthesis; Chlorophyll biosynthesis.
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89123059; PubMed-2492501;
Adams C.W., Forrest M.E., Cohen S.N., Beatty J.T.;
"Structural and functional analysis of transcriptional control of the Rhodobacter capsulatus puf operon.";
J. Bacteriol. 171:473-482(1989).
-I- FUNCTION: REQUIRED FOR BACTERIOCHLOROPHYLL BIOSYNTHESIS. DIRECTLY INVOLVED IN THE ASSEMBLY OF BOTH THE B875 AND B800-850 PIGMENT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-88169603; PubMed-3127391;

Bauer C.E., Young D.A., Marrs B.L.;

*Analysis of the Rhodobacter capsulatus puf operon. Location of the coxygen regulated promoter region and the identification of an additional puf-encoded gene. *;

J. Biol. Chem. 263:4820-4827(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter.
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                                                                                                    5 GSQHID 10
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SIMILARITY: BELONGS TO THE PUFQ FAMILY.
                                                                GVQHVD
                                                                                                                                                       Similarity
                                                                    15
                                                                                                                                        Conservative
                                                                                                                                                       41.9%;
66.7%;
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Last annotation update)
                                                                                                                                   Score 26; DB 1;
Pred. No. 2.8e+02;
1; Mismatches 1
                                                                                                                                                                       DB 1; Length 74;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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   score q
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_amamal:*
7: sp_mhc:*
8: sp_organe1]
9: sp_hage:*
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11: sp_rodent
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17: sp_arche
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Match
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Gapop 10.0 ,
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62
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Copyright (c) 1993 - 2002 Compus
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sp_bacteriap:*
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sp_unclassified:*
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019274
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Q9U194
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Q37764
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Q97QB1
Q97PZ4
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                                                       Q96ht2 homo sapien
Q37764 mytilus edu
Q377764 mytilus edu
Q99yi8 rattus norv
Q97gb1 streptococc
Q97pz4 streptococc
Q97pz4 streptococc
Q99ma0 sus scrofa
Q9u194 leishmania
Q9u194 leishmania
Q9u194 salmonella
Q91293 pseudomonas
Q84884 salmonella
Q96hy2 homo sapien
062344 caenorhabdi
Q9m4h3 vitts vinif
019274 saguinus oe
Q15962 homo sapien
Q9bnh0 amblyomma s
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ALIGNMENTS

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RESULT 1
Q96HT2
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Best Local S
Matches 7
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Q95HT2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                          037764 PRELIMINARY; PRT; 99 AA. 037764; 037764; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TREMBLREL. 19, Last annota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC008122; AAH08122.1; -.
SEQUENCE 79 AA; 8413 MW; B61779A1A472913B CRC64;
COI.
Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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77.8%;
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Pred. No.
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RESULT 3
Q9QYJ8
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Best Local S
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01-MAY-2000 (TIEMBLIEL 13, Last sequin-
01-DEC-2001 (TIEMBLIEL 19, Last anno-
DECAY ACCELERATING FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics 131:397-412(1992).

-II- EUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE FIGURATION OF OXYGEN TO WATER. S
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. S
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I I
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING I
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF
                                                                                                                                                                                                                           MEDLINE-20130146; PubMed-10663575;
Miwa T., Okada N., Okada H.;
"Alternative exon usage in the 3'region of a
glycosylphophatidylinositol-anchored and tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INNER MEMBRANE (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL; M83762; AAA31914.1; -.
EMBL; M83763; AAA31913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                          decay-accelerating factor.";
Immunogenetics 51:129-137(2000).
EMBL; AB026905; BAA88994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00115; COX1; 1.
Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
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                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                             STRAIN-WISTARST;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
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COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).

PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND COPPER B (BY SIMILARITY).

CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C +
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  Similarity
5; Conserv
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6; Conser
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                       53.2%;
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genome organization
                                                                                            MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown
Score 33; DB
Pred. No. 60;
3; Mismatches
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                                                                                            B822DC894E684593
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Pred. No.
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Best Local S
Matches 6
                                                                                                                                                                                                                                      Q97PZ4;
Q97PZ4;
01-OCT-2001
01-OCT-2001
01-DEC-2001
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angluoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21357209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen T.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Levis M.R., Radune D.,
HOltzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                            STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
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01-DEC-2001
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EMBL; AE007429; AAK75412.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae.
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1 (TrEMBLrel. 18,
1 (TrEMBLrel. 19,
7 ELEMENT, ORF1.
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1 (TrEMBLrel. 18,
1 (TrEMBLrel. 19,
2 ELEMENT, ORF1.
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micutes; Bacillus/Clostridium group;
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Last annotation updat
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62;
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Best Loc
Matches
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01-MAR-2001 (TrEMBLrel 16, C

01-MAR-2001 (TrEMBLrel 16, I

01-JUN-2001 (TrEMBLrel 17, I

CD5 ANTICEN (FRAGMENT).

Sus scrofa (Pig).
               SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
Hilbert H., Wedler H.
Lawson D., Quail M.,
Submitted (JUN-2000)
                                                                                                Q9U194 PRELIMINARY; PRT; 93 AA.
Q9U194;
01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
HYPOTHETICAL 10.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-08251471; PubMed-9589566;
Appleyard G.D., Wilkie B.N.;
Appleyard G.D., Wilkie B.N.;
Porcine CD5 gene and gene product identified on "Porcine CD5 gene and gene product identified on species conserved cytoplasmic domain sequences.";

species conserved cytoplasmic domain sequences.";
                                                                                                                                                                                                                                                                                NON_TER
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Science 293:48-506(2001).
Science 293:484; AAK75537.1;
TIGR; SP1443; -.
Complete proteome.
                                                                    Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Appleyard G.D., Wilkie B.N.;
Submitted (AUG-2000) to the
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Submitted (AUG-2000) to the EMBL; AF291867; AAG02103.1;
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
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5; Conser
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79 AA;
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73
AA;
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                                                                                                                                                                                                                                                                        8144 MW;
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                 Rajandream M.,
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41.7%;
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                                                                             Kinetoplastida;
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Last annotation update)
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                 EMBL/GenBank/DDBJ
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Pred. No. 89;
4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                        82DBD6D10F9B58B8
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                          Duesterhoeft A., A., Barrell B.G.
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62;
                                                                             Trypanosomatidae;
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ina; Suidae;
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Best Local
SEQUENCE FROM N.A. STRAIN-ATCC 15692 , MEDLINE-20437337; I Stover C.K., Pham )
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NON_TER
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
REVERSE TRANSCRIPTASE-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FQI8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ivens A.C., Lewis S.M., Bagherzade Smith D.F.;
Smith D.F.;
A physical map of the Leishmania Genome Res. 8:135-145(1998).
EMBL; AL117319; CAB55518.1; -.
Hypothetical protein.
                                                  Pseudomonas.
NCBI_TaxID=287;
                                                                                                               Q91293;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2001 (TrEMBLrel. 18,
                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                    retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AF232993; AAG44333.1; ...
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TRANSPOSON-COPIA-LIKE
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                                                                                                       HYPOTHETICAL PROTEIN
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/ PAO1;
PubMed=10984043;
X.-Q.T., Erwin A
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50.0%;
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1; Mismatches
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 A.L.,
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 Mizoguchi
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Q96HY2
ID Q96HY
AC Q96HY
AC Q96HY
AC Q1-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT UNKNO
OS HOMO
OC EUKAI
OC MAMMMA
OX NCBI,
RN [1]
RN [1]
RR SEQUE
RA STrau
SQ SEQUE
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ID O8488
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DT SIGNA
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EMBL; AE004628; AAGO5409.1; -
EMBL; AE0046287 AAAGO5409.1; -
EMBL; AE0046287 AAAGO5409.1; EDCE3FF490CID520 CRC64;
                                                                                                                                           Q96HY2 PRELIMINARY; PRT; 58 AA. Q96HY2; Q1-DEC-2001 (TrembLrel. 19, Created) 01-DEC-2001 (TrembLrel. 19, Last sequence up 01-DEC-2001 (TrembLrel. 19, Last annotation UNKNOWN (PROTEIN FOR MGC:15178).
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SEQUENCE
       Submitted (MAY-2001) to the EMBL; BC007973; AAH07973.1; SEQUENCE 58 AA; 6728 MW;
                                          SEQUENCE FROM N.A.
TISSUE-MUSCLE, AND
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                             NCBI_TaxID=9606;
                                                                                                                                   Homo sapiens (Human).
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Submitted
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01-NOV-1998
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hage genes in Salmonella.";
tted (JUN-1998) to the EMBL
AF001386; AAC26063.1;
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1998 (TremBLrel. 08, Last a
FACTOR REGULATORY PROTEIN
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Primates;
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Catarrhini; Hominidae;
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No. 1.1e+02;
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Q9M4H3;
Q1-OCT-2000
01-OCT-2000
01-OCT-2000
                           during grape berry ripening. Cloning an encoding putative cell wall and stress plant Physiol. 122:803-812(2000).

EMBL; AJ237990; CAB85630.1; -.
SEQUENCE 65 AA; 6777 MW; B5EA7D8D7E
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                            Davies C., Robinson S.P.;
"Differential screening indicates a dramatic change in mRNA and characterization of a dramatic change in mRNA arriver arrange berry ripening. Cloning and characterization of a dramatic change in mRNA arriver arrange proteins.";
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EMBL; Z81577; CAB04648.1; -.
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                     STRAIN-CV. SHIRAZ; TISSUE-FRUIT;
MEDLINE-20177861; PubMed-10712544;
Davies C., Robinson S.P.;
                                                                                                                                                                   Vitis vinifera
Eukaryota; Viri
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AA; 6997 MW;
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1.2e+02;
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1.1e+02;
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RESULT 15
Q15962
ID Q1596
AC Q1596
AC Q1596
DT Q1-NO
DT Q1-NO
DT G1-NO
DT G1-WARO
OC HOMO
OC EUKAR
OC MARMMA
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RN [1]
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RP SEQUE
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ID 01927

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InterPro; IPR000353; MHC_II_beta; 1.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC II; Transmembrane NON_TER 83 83
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O19274;
O19274;
O19274;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 105, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC CLASS II ANTIGEN (FRAGMENT).
Saguinus oedipus (Cotton-top tamarin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-93103017; PubMed-8416675;

Peelle M.E., Carr F.E., Baker J.R.Jr., Wartofsky L., Burman K.D.;

"TSH beta subunit gene expression in human lymphocytes.";

Am. J. Med. Sci. 305:1-7(1993).

EMBL; S51112; AAB24571.2; -.

HSSP; P01233; 1XUL.

InterPro; IPR000359; Cys_knot.

InterPro; IPR001545; Glyco_hormone_beta.

Pfam; PF00007; Cys_knot; 1.
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI_TaxID=9606;
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STRAIN-B95-8; TISSUE-BLOOD;

MEDLINE-97525963; PubMed-9098421;

Bidwell J.L., Lu P., Wang Y., Zhou K., Clay T.M., Bontrop R.E.;

"DRB, DOA, DQB and DPB nucleotide sequences of Saguinus oedipus B95-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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STRAIN-B95-8; TISSUE-BLOOD;
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4; Conservation
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SEQUENCE 87 AA; 9911 MW; 13AEEE7F9728D
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Cholera toxin B/en CTP3 epitope of the Cholera toxin B an Cholera toxin B/en E. coli heat labil Residues 50-64 of Sequence of amino Network polymer wh Sequence of amino ADP-ribosylating t
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12	22	22	22	22	22	22	22	22	22	22	21	21	19	17	10	22	22	11	22	22	22	22	22	19	17	17	17	17	σ	22	21	20	20
AAR12630	AAB62372	AAB62380	AAB62378	AAB62376	AAB62375	AAB62373	AAB62368	AAB62363	AAB62359	AAG65992	AAY96872	AAY96652	AAW59770	AAW06605	AAP93561	AAB62377	AAB62374	AAR04163	AAB62369	AAB62379	AAB62370	AAB62367	AAB62365	AAW80808	AAW06607	AAW06606	AAR94939	AAW04857	AAP50340	AAB66239	36	9522	AAY41816
GtfB.1/CTB chimeri	coli LTB	i LTB	i LTB prote		LTB	i LTB	V. cholera cholera	V. cholera cholera		Cholera toxin B su	Plant-optimized V.	Plant-optimized E.	Amino acid sequenc	Cholera toxin B su	B subunit of the h	E. coli LTB protei	E. coli LTB protei	Cholera Toxin B-su	V. cholera cholera	E. coli LTB protei	V. cholera cholera	V. cholera cholera	V. cholera cholera	Amino acid sequenc	Cholera toxin B su	Cholera toxin B su	Heat labile entero	Synthetic cholera	Sequence of sub-un	E coli verotoxin-1	2	t	Escherichia coli v

ALIGNMENTS

RESULT 1 AAY87461

AAY87461 standard; peptide; 12

A

Cholera toxin B/enterotoxin B-derived peptide,

SEQ ID NO:3.

EtxB;

03-JUL-2000 AAY87461;

(first entry)

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Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                    Vibrio cholerae.
Escherichia coli.
                            WPI; 2000-256943/22.
                                           Williams NA, Hirst TR;
                                                                         07-SEP-1998;
                                                                                        07-SEP-1999;
                                                                                                                     WO200014114-A1.
                                                         (UYBR-) UNIV BRISTOL.
                                                                                                        16-MAR-2000
                                                                        98GB-0019484.
                                                                                        99WO-GB02970.
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Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind glycolipid receptor GM-1 -

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RESULT 2
AAP93498
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Best Local S
Matches 12
                                                                                                                                        epitope, and expressed of antibodies
This sequence corresponds subunit. The DNA sequence
                                                                              Disclosure; fig.4B; 137pp; English.
                                                                                                                                                            New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn.
                                                                                                                                                                                                                                                    WPI; 1989-356496/48.
N-PSDB; AAN92414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-NOV-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTP3 epitope of Cholera toxin B subunit; flagellin fusion vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 15;
                                                                                                                                                                                                                                                                                                                                     Marjarian WR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTP3 epitope of the Cholera toxin B subunit.
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                                                                                                                                                                                                                                                                                                                                     Stocker BAD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
to the CTP3 epitope of the Cholera toxin encoding this ligates to othersynthetic
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Matches 12
                                                                                                                          A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AARB5126-30 and esp. AARB5125), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for
                                                                                            Sequence
                                                                                                                                                                                                                         Claim 7; Page 25; 40pp; English
                                                                                                                                                                                                                                                  aldehyde
                                                                                                                                                                                                                                                            Vaccines for oral immunisation against infecting agents, e.g cholera - comprise a conjugate of an antigen of an infecting covalently bound to micro:particulate inert carrier, e.g. mo
                                                                                                                                                                                                                                                                                                           WPI; 1995-403805/51.
                                                                                                                                                                                                                                                                                                                                  Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; antibodies; secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR85125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR85125 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy.
                                                                                                                                                                                                                                                                                                                                                                                 03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09529701-A1
                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1996
                                             Local Similarity es 12; Conserv
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           VEVPGSQHIDSQ 12
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VEVPGSQHIDSQ
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12; Conser
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                                                                                                                  IgA class.
                                                                                                                                                                                                                                                                                                                                  Mirelman
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                                             Conservative
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                                                                                             AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B antigenic peptide fragment CTP3.
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                                                          Score 62;
Pred. No.
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Pred. No.
                                             Mismatches
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. 5.9e-05;
ches 0;
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                                                                      DВ
                                             .9e-05;
s 0;
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RESULT 4
ANASSULT 4
ANASSULT 4
ANASTA462
ANAST
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                                                                                                                          Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                   is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (ETXB and CtXB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of EtX and CtX, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtXB and/or CtXB, exerting the same effects as normal EtXB and CtXB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-4-alpha-2 loop; GM-1 ganglioside receptor; adjuvant; immune disorder; diarrhoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                              particularly preferred.
                                                                                                                                                                                                                                                                                                                                            represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                        Local
6
                                                     1 VEVPGSQHIDSQ 12
                                                                                                                       l Similarity
12; Conserv
                                                                                                                                                                                                                                                     21
                                                                                                                          Conservative
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                                                                                                          100.0%; sc.
100.0%; Pr
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                                                                                                                Score 62; DB zi,
Pred. No. 8.6e-05;
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                                                                                                                                                                                Length
                                                                                                                       Indels
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                                                                                                                                                                                      21;
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RESULT 5
AAY87463
ID AAY8

AAY87463 standard; peptide;

21

18-MAR-1996 AAR76748;

(first entry)

AAR76748 standard; Protein; 23

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RESULT 6
AAR76748
ID AAR7
XX
AC AAR7
XX
DT 18-M
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                                                                                                                                                                                                                                                                                                                  The invention relates to peptide fragments of the Escherichia coli heat clabile enterotoxin (Etx) and its closely related homologue, cholera coxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the same effects as command EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition commune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 crepresent preferred peptides of the invention, AAY87460 being composition constants.
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside readjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycolipid receptor GM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams NA, Hirst TR;
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                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                             particularly preferred.
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                                                                                                                                                 VEVPGSQHIDSQ
                                                                                                                                                                                                                12;
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                 17
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                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                             Score 62; DB 21;
Pred. No. 8.6e-05;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor; immunomodulation;
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                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                            Length 21;
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RESULT 7
AAP30265
ID AAP3
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                                                                                                                                                            В
                                                                                                                                                                                        This sequence is encoded by a fragment of the the plasmid pLPA93
which was used in the production of fimH fusion genes comprising
the cholera toxin B subunit inserted into the fimH gene. This insert
shows the inclusion of the B subunit into the FimH grotein at position
224-226. The chimeric genes were then opt. further modified by insertion
of the hepatitis B virus surface antigen pre-S2 region into a different
position of the FimH adhesin of type I fimbriae. Restiction site handles
(BglII-sites) were introduced into the fimH gene, and the foreign
epitopes are then inserted in-frame. In the selected positions the
insertion of the epitopes did not significantly alter the adhesive
function of the FimH protein. The expression of the chimeric proteins
on the surface of fimbriae on bacterial hosts illustrated the possibility
of using bacterial adhesins as general presenters of foreign antigens and
epitopes. These chimeric genes may be used in the production of variant
fimH adhesins which may be useful for targetting active compounds
the adhesins which may be useful for targetting active compounds
                                                                                                            Matches
                                                                                                                         Best
                                                                                                                                   Query Match
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Chimeric
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FimA;
AAP30265 standard; Protein;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1994;
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                                                                        VEVPGSQHIDSQ
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FimF;
                                                                                                           l Similarity
12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                 specific bacterial adhesins - uses and microbial cells to locations
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                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                        Page 58; 152pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klemm P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYSTEMS
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                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fimbriae; organelle; adhesin; alpha-D-mannoside
fimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                            AA,
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23
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                                                                                    12
                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Represents FimH residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Linker
                                                                                                                                  .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxin B subunit and FimH
                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                            0
                                                                                                                      Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pallesen
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                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
ions of
                                                                                                                       DB 16;
9.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit 50-64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sokurenko
                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 for targetting receptors
                                                                                                                                   Length
                                                                                                            Indels
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                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            active
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RESULT 8
AAP50439
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                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                              without carriers. Unit dose a vaccine 1-10mg of active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                Synthetic
                                                      Heat-labile
                                                                           Network polymer labile toxin (L7
                                                                                                             01-JAN-1980
                                                                                                                                    AAP50439;
                                                                                                                                                          AAP50439 standard; protein;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of amino acids 50-75 of the carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1983;
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12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                              100.0%; llarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raulais D,
                                                      enterotoxin;
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                                                                                                             (first entry)
                                                                          ler which comprises a series
(LT)/heat-stable toxin (ST)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rivaille
                                                      heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                 cpd.
                                                                                                                                                           41
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                        Score 62;
Pred. No.
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                                                                                                                                                                                                                                                               Mismatches
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                                                                          of composite polypeptide r
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                                                                                                                                                                                                                                                                                   Length 26;
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                                                                                         coli heat-
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RESULT 9
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XX Netw
DE Netw
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XX Heat
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XX WO85
XX I2-1
XX I
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Best Local
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The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cy of the repeating units. This polypeptide may be used in
                                                                                                                                                                                                                               WPI;
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                                                                                                                                                    New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8502611-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Network polymer which comprises a series of composite E. coli labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP50436 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houghten RA;
                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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12; Conser
                                                                                                    Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxin;
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                                                                                                    100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                         83US-0559469
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Pred. No.
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxin(s)
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                                Cys residues
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                                                                                                                                                                                                                        Cholera toxin B, sub-unit polypomedicaments - effective against cholerae infections, are prepd.
                                                                      administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                         The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of,
                                                                                                                                                                                                                                                                                                                                    (CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination of mammals for protection against the enterotoxins. composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. Yels Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                    and vaccination against, cholera infections and animal and human infections due to {\tt E.} coli (enterotoxin LT). The medicament may l
                                                                                                                                                                                                                                                                                                                                                                                                                                           EP95426-A.
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                                               Sequence
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1 Similarity 100.0%;
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12; Conserv
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PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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             100.
           .0%;
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             Score 62;
Pred. No.
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Pred.
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red. No. 0.00021;
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                        Length 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                              Dodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B1 subunit which
                                                                                                                                                                                                                                       and
Vibrio
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                                                                                                                     þe
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RESULT 12
AAY41816
ID AAY41
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AAR72545
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                                                                                                                                                                                                  Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-)
                                                                                                                                                                                                                                                                           AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            active site; E. coli
Bordetella pertussis
  ADP-ribosylating toxin; PT; three-dimensional structure;
                                  Escherichia coli verotoxin-1 B-subunit.
                                                                            AAY41816;
                                                                                                                                                                                                                                                                                                                                                                                                   crystalline
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-132623/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0omen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP646599-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72545 standard;
                                                        08-DEC-1999
                                                                                                  AAY41816
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                     pertussis
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              New modified forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Armstrong GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP-ribosylating toxin (verotoxin-1 B-subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-1995
                                                                                                                                                         40
                                                                                                                                                                              1 VEVPGSQHIDSQ 12
                                                                                                                                                         VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                         molecules
                                                                                                                                                                                                   l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNAUGHT LAB LTD
UNIV ALBERTA.
                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GD, Cockle SA,
Read RJ, Stein
                                                                                                                                                                                                                                                                     infection.
                                                                                                                                                                                                                                               93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 forms
                                                                                                                                                                                                   Conservative
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94EP-0306219
                                                                                                                                                                                                                                                                                                                                                                                                 s of pertussis holotoxin - developed using of pertussis holotoxin and its complexes
  structure;
                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hazes B,
crystalline pertussis holotoxin;
; LT; immunoprotective; infection.
                                                                                                   93
                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                  Score 62; DB Pred. No. 0.0; Mismatches
                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein
                                                                                                                                                                                                   0.00045;
                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , HM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loosmore
                                                                                                                                                                                                                        Length
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                         93;
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                                                                                                                                                                                                                                                                                                                                                                                                   with
                                                                                                                                                                                                   0;
            ETA;
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                                                                                                                                                                                                   RESULT 13
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(1) identification of at least one amino acid (aa) residue of the crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to perduce the modified holotoxin. This method is used for modifying certussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin can be identified. This can be used to predict (aa) which contribute to the toxicity of the holotoxin to produce
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                     Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                          E. coli heat-labile
                                                                                                                                                AAW95226;
                                                                                                                                                                         AAW95226 standard; peptide; 93
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONN-) (
                           heat-labile;
                                                                                                                                                                                                                                                                                                                                                                                         immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating besident peptide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5965385-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                      16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 5; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hazes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В В,
                                                                                                                                                                                                                                            VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNAUGHT LAB
UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                      (first
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93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        producing modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0467974
                                                                                                                                                                                                                                             51
                                                                                          toxin (LT) beta-subunit sequence
                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cockle SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                              Score 62;
Pred. No.
                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pertussis
                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                 DB 20;
.00045;
s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           holotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein
                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MH,
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                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                            toxin
                                                                                                                                                                                                                                                                                                 Gaps
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Escherichia

coli

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RESULT 14
AAY68365
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure of PT have functional and/or structural resemblance to other bacterial toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present sequence represents the beta-subunit of LT toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Armstrong
Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods of preparing a pertussis holotoxin (PT having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of the comprise of the comprise of the comprise of the compression of the compressi
                                                                                                          US6018022-A
                                                                                                                                                                                                                                                                                    Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                Heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY68365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY68365 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105104/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    labile toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GD, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                              coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cockle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0292968.
93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    B subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e SA,
Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 0%;
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PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В,
                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ).00045;
es 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. ANY68340 to ANY68385 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crystalline form of isolated pertussis holotoxin useful proteins which have functional resemblance -
                                                                               21-MAY-1998;
                                                                                                        02-JAN-2001.
                                                                                                                                                     Escherichia coli
                                                                                                                                                                                        Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor;
                                                                                                                                                                                                                            E coli verotoxin-1 B
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                                                                                                                                                                                                                                                                           AAB66239;
                                                                                                                                                                                                                                                                                                  AAB66239 standard; Protein;
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12; Conserv
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Oomen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention.
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                                                                                                                                                                                                                                                  (first entry)
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93US-0110947.
94US-0251121.
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93US-0110947.
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                                                                                98US-0082514
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(CONN-) CONNAUGHT LAB LTD

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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin. Pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
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40 VEVPGSQHIDSQ 51
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
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US-08-467-976-26
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US-08-952-337-6
US-08-952-337-2
US-09-191-852-21
PCT-US95-13376-21
US-08-952-337-1
US-08-952-337-2
US-08-952-337-2
US-08-952-337-2
US-08-829-0268-6
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US-08-829-0268-6
US-08-829-0268-6
US-08-829-0268-6
US-08-8747-810-2
US-08-8747-8710-2
US-08-8748-989-2
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(without alignments)
41.388 Million cell updates/sec
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Patent No.
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Sequence 14, Appl	Sequence 3, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 3, Appli	Sequence 22, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 1, Appli	Patent No. 5194375

ALIGNMENTS

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; TYPE: amino acid
H: 93
CHARACTERIS
ORMATION
; TELEFAX: (416) 595-1163
; TELEPHONE: (416) 595-1155
; FELECOMMONICATION INFORMATION:
REFERENCE/DUCKET NUMBER: 1030-300
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· FILING DAME: 31-MAY-1994
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CONTRACTOR DAMA.
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7.
CLASSIFICATION DAMA.
APPLICATION NUMBER: US/08/292.968
LICATION DATA:
'n
; OPERATING SYSTEM: PC-DOS/MS-DOS
B
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; ZIP: M5G 1R7
; COUNTRY: Canada
; STATE: Ontario
; CITY: Toronto
; STREET: Suite 701, 330 University Avenue
m & McBurr
G
; NUMBER OF SEQUENCES: 46
NVENTION
HAZES, Bart
: ARMSTRONG, Gl
: KLEIN, Mic
: LOOSMOR
: OOMEN, F
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; APPLICANT: READ, Randy J.
; GENERAL INFORMATION:
; Patent No. 5856122
; Sequence 26, Application US/08292968
US-08-292-968-26

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                                                          Query Match
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Patent No.
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APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
APPLICATION NUMBER: US 08/110,947
                                                                                                                                                               TELEFAX: (416) 595-116: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,97
FILING DATE:
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                        NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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                                            Local Similarity
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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CITY: Toronto
                                                                                                         TOPOLOGY:
                                                                                                                                                  LENGTH:
                                                                                                                                                                                                              TELEPHONE:
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1 VEVPGSQHIDSQ 12
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l2; Conservative
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                                                                                                                                                  93 amino acids
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                            100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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                                                                                                      linear
                                                                                                                                                                                                              (416) 595-1155
                                                                                                                                                                                                                                                                                                     UMBER: US 08/110,947
24-AUG-1993
                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODIFICATION OF PERTUSSIS TOXIN
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                          Score 62; DB 2;
Pred. No. 0.00032;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 2;
Pred. No. 0.00032;
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                                                        Length 93
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RESULT 4
US-08-467-976-26
; Sequence 26, Application US/08467976
; Patent No. 6018022
; GENERAL INFORMATION:
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US-08-467-536-26
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
ADME: STEWARD MIGHTS 11
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REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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APPLICATION NUMBER: US 0
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                              40
                                                                                                                                                                                                                                                                      LENGTH: 93 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                           1 VEVPGSQHIDSQ 12
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40 VEVPGSQHIDSQ 51
                                                                                                                                                                           Local Similarity 100 es 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite 701,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEIN, Penelope E. COCKLE, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAZES, Bart
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OOMEN, Raymond F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER: US/08/467,536
06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 08/292,968
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                                                                                                                                                                           Score 62; DB 2;
Pred. No. 0.00032;
; Mismatches 0;
                                                                                                                                                                                                       Length 93;
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RESULT 5
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                                                                                                                                                                Sequence 26
Patent No.
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APPLICATION NUMBER: US U8/4-1,

FILING DATE: 31-MAY-1994

PRIOR APPLICATION DATE: US 08/110, 9

APPLICATION NUMBER: US 08/110, 9

FILING DATE: 24-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: STEWART Michael I.

NAME: STEWART NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNIA...
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOMPUTER: IBM PC compatible
TOMPUTER: TOMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1038-453 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
REORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                        40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                     1 VEVPGSQHIDSQ 12
                                                                                                                                                                    26, Application US/09082514
). 6168928
                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sim & McBurney
Suite 701, 330 Un:
                                             OOMEN, Raymond P.
KLEIN, Michel H.
ARMSTRONG, Glen D.
                                                                                              READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
                                 HAZES, Bart
                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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   MODIFICATION OF PERTUSSIS TOXIN 46
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Pred. No. 0.00032;
; Mismatches 0;
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; LENGTH: PRT
; ORGANISM: Vibrio cholerae
US-08-952-337-5
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                                                  Best Loc
Matches
                                                                                Query Match
                                                                                                                                                                               SOFTWARE: 1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 3846/0D758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                Local Similarity
les 12; Conserv
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ZIP: M5G 1R7
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1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                              FastSEQ for Windows Version 3.0
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                                          100.0%;
milarity 100.0%;
Conservative 0;
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Pred. No. 0.00032;
0; Mismatches 0;
                                               Score 62; DB 3;
Pred. No. 0.00036;
Mismatches 0;
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VEVPGSQHIDSQ

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; APPLICANT: Holmgren, Jan
; APPLICANT: Lebens, Michael R.
; TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
; TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
; FILE REFERENCE: 3846/DD758
; CURRENT APPLICATION NUMBER: US/08/952,337
; CURRENT FILING DATE: 1998-01-05
; EARLIER APPLICATION NUMBER: PCT/SE96/00570
; EARLIER APPLICATION NUMBER: SE 9501682-0
; EARLIER APPLICATION NUMBER: SE 9501682-0
; EARLIER FILING DATE: 1995-05-05
; EARLIER FILING DATE: 1995-05-05
; EARLIER FILING DATE: 1995-05-05
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Best Local Similarity 100.
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Holmgren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-115
                                                                         APPLICATION NUMBER: US 00 FILING DATE: 23-FEB-1995 ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                          APPLICATION NUMBER: US/08/472,171 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
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5. 5932714
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                                                                                                                                             US 08/393,334
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                                       1038-507 MIS:vg
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Pred. No. 0.00036;
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RESULT 10 US-09-013-047-2

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                                                                                                                       US-08-894-526-2
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                                                           Query Match
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Matches 12
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Best Local S
Matches 12
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GENERAL INFORMATION:
APPLICANT: LOOSMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2,
                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION UNMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                    LENGTH: 103 amino
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yacoob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Klein, Michel H
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LENGTH: 103 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ontario
COUNTRY: Canada
                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 01-DE
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
50 VEVPGSQHIDSQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: Canada ZIP: M5G 1R7
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               1 VEVPGSQHIDSQ 12
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amino acid
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                                                           Conservative
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h Floor, 330 University Avenue
                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                     01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSION OF GENE PRODUCTS FROM GENETICALLY MANIPULATED STRAINS OF BORDETELLA
                                                                       100.0%;
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Pred. No.
                                                                       Score 62; DB 2;
Pred. No. 0.00036;
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hes 0;
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RESULT 11
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                                                                                                                                                                                              Sequence 2, Application US/09374597 Patent No. 6140082
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                            GENERAL INFORMATION:
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                                                  TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
                                                                                                     APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                      CORRESPONDENCE ADDRESS
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FILING DATE:
CLASSIFICATION:
     STREET:
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REFERENCE/DOCKET NUMBER: 10:
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                     ADDRESSEE:
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M5G 1R7
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E: Sim & McBurney
330 University Avenue, 6th Floor
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                                                                                                                                                           Loosmore, Sheena M.
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Pred. No.
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US-09-191-852-21
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Patent No. 6194560
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Fox, David 1.
                                                                                                 PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: FEBRUAR
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                                 APPLICATION NUMBER: PCT/
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/8
FILING DATE: 04-AUG-1997
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CITY: Houston
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les 12; Conserv
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ZIP: M5G 1R7
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1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                   Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
VENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
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Pred. No. 0.
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NAME: FOX, David L. REGISTRATION NUMBER:

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RESULT 14
US-08-952-337-1
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US-09-191-852-21
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PCT-US95-13376-21
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Best Local :
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Best Local Similarity 100.0%;
Matches 12; Conservative (
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 0.
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
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LENGTH: 103 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                        50 VEVPGSQHIDSQ
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REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36
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ZIP: 77027-9095
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TYPE: amino acid
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les 12; Conserv
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Pred. No. 0.00036;
); Mismatches 0;
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Pred. No. 0.00036;
; Mismatches 0;
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SOUTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 123 TYPE: PRT ORGANISM: Eschcerichia coli
Search completed: October 24, Job time: 8.08197 secs
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; ORGANISM: Vibrio cholerae
US-08-952-337-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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Best Local Similarity
Matches 12; Conserv
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                                                                               Matches
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APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
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                                                                        70 VEVPGSQHIDSQ
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o. 6019973
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ilarity 100.0%;
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Pred. No.
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Pred. No. 0.00044;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: /cgn2_6/ptodata/1/paa/I
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Copyright (c) 1993 - 2002 Compugen Ltd.
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(without alignments)
52.114 Million cell updates/sec
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Score	Match	Length I	₩	ID	Description	
62	100.0		21	US-09-786-648-3	Sequence 3,	
62	100.0		11	US-08-732-371-1	Sequence 1,	
62	100.0		11	US-08-732-371A-1	Sequence 1,	App
62	100.0		21	US-09-786-648-4	Sequence 4,	App
62	100.0		21	US-09-786-648-5	Sequence 5,	App
62	100.0		5	US-08-110-947-10	Sequence 10,	App
62	100.0	93	ū	US-08-110-947A-26	Sequence 26,	App
	SCOTE 622 622 622 622 622 622 622 622 622 62			Match Length DB 100.0 12 21 100.0 15 11 100.0 15 11 100.0 15 12 100.0 21 21 100.0 21 21 100.0 93 5		Match Length DB ID 100.0 12 21 US-09-786-648-3 100.0 15 11 US-08-732-371-1 100.0 15 11 US-08-732-371A-1 100.0 15 11 US-09-786-648-4 100.0 21 21 US-09-786-648-5 100.0 21 21 US-09-786-648-5 100.0 93 5 US-08-110-947A-26

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PCT-US99-17130-318	TO# 1/1 00	-60-171-181-	-69-	-09-	6	-09-786-6	-09-252-9911	-09-816-660-18876	-09-	-60-324-109	-09-134-000	-09-252-991	-09-402-100-	•	- 1	٠	US01-08582-	us01-08582-	09-760-234-	1	US-08-784-218-6	8-150-305A-3	09-756-983-	09-756-983-	09-756-983	08-914-4791	-08-914-479-2	09-470-124-	09-470-124-5	US99-30747-5	-US99-3074	09-836-433-	Ψ	US-09-836-433-14	17-906-	S-08-782-832-	-80-	US-08-251-121-26
Sequence 318, App	100	1503	46	43	47		17		18876,	19962,		292		2		e 2,	4,	ω	7,	տ	6	'n	22,	18,	15	2	2,	57	е 55,	Sequence 57, Appl	55, 1	22,	20,	14,	21,	e 15	Sequence 2, Appli	26,

ALIGNMENTS

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US-09-786-648-3
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SOFTWARE: MS DOS
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
FILE REFERENCE: 7438
                                    Query Match 100
Best Local Similarity 100
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                  LENGTH: 12
TYPE: PRT
ORGANIAM: E. coli
FEATURE:
LOCATION: 50...61
OTHER INFORMATION: human variant E. coli
COTHER INFORMATION: human variant E. coli
1 VEVPGSQHIDSQ 12
                                                         100.0%;
                                        0;
                                                     Score 62; DB 21;
Pred. No. 0.00041;
                                        Mismatches
                                                                         Length 12;
                                        Indels
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US-08-732-371-1
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US-08-732-371A-1
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Best Local S
Matches 12
                                                                                                Sequence 1, Application US/08732371A
GENERAL INFORMATION:
APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S,
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: INFECTING AGENTS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109519
ETILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: MIRELM
REFERENCE/DOCKET NUMBER: MIRELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: INFECTING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/732,371 FILING DATE: 09-JAN-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 419 Sever CITY: Washington STATE: D.C.
                             STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
COUNTRY:
                  STATE:
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l Similarity 100.0%;
l2; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
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                D.C.
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419 Seventh Street, N.W., Suite 300
                                                  419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 202-628-5197
202-737-3528
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                                                                    BROWDY AND NEIMARK
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                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 11;
Pred. No. 0.00053;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
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LOCATION: 45...65; OTHER INFORMATION: OTHER INFORMATION: US-09-786-648-4
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US-09-786-648-4
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                                                                  Query Match
Best Local S
Matches 12
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LENGTH: 21
TYPE: PRT
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APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/786,648 CURRENT FILING DATE: 2001-03-07 PRIOR APPLICATION NUMBER: PCT/GB99/02970 PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                            ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Relicurrent APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TYPE: a
                                                                    Local Similarity
nes 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%; Score 62; DB 11; Local Similarity 100.0%; Pred. No. 0.00053; les 12; Conservative 0. Minmain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
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                                  1 VEVPGSQHIDSQ 12
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VEVPGSQHIDSQ 17
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OGY: linear
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                                                                      Conservative
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                                                                                     Score 62; DB 21;
Pred. No. 0.00079;
                                                                        Mismatches
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RESULT 5 US-09-786-648-5

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                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
NAME: FALLOW, Charles W
REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 21
TYPE: PRT
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APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: LOCATION: 45...65
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable OTHER INFORMATION: porcine E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: E. coli
                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/110,947 FILING DATE: 24-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: Suite 1203 Crystal Plaza I, 2001 Jefferson
STREET: Davis Hwy.
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                    LENGTH:
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                 : 93 amino acids amino acid
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KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEIN, Penelope E
COCKLE, Stephen A
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Pred. No.
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0.00079;
hes 0;
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APPLICANT:
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; TOPOLOGY: US-08-110-947-10
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US-08-251-121-26
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US-08-110-947A-26
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                                                                  Sequence 26, Application US/08251121 GENERAL INFORMATION:
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 415-0813
TELEFAX: (703) 415-0813
TELEFAX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/110,947A
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STEIN, Penelope E APPLICANT: COCKLE, Stephen A APPLICANT: OOMEN, Raymond P APPLICANT: KLEIN, Michel H
                                                 APPLICANT:
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                    LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite 1203 Cr
STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 VEVPGSQHIDSQ 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FALLOW, Charles W REGISTRATION NUMBER: 28,946
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                                                                                                                                                                                    1 VEVPGSQHIDSQ 12
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STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
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                                                    READ, Randy J.
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                                                                                                                                                                                                                                   Score 62; DB 5;
Pred. No. 0.0044;
Mismatches 0
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Pred. No. 0.0044;
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                                                                                                                                                                                                                                                                   Length 93;
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                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Applicati
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-110 INFORMATION FOR SEQ ID NO:
                                          COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWARR, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-335
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 00 FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: STEWART, Michael I
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                 SOFTWARE:
                                                                                                                                                 STATE: Ontario
                                                                                                                                                                      CITY: Toronto
                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 VEVPGSQHIDSQ 51
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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               APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        Application US/08393334
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                                                                                                                                                                                     E: Sim & McBurney
330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sim & McBurney
Suite 701, 330 University Avenue
                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                          Loosmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canada
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NUMBER:
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US/08/393,334
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Pred. No. 0.0044;
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RESULT 10
US-08-782-832-15
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                                                                US-08-782-832-15
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 Best Local
Matches 1
                              Query Match
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Best Local :
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                                                                                                                                       TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Mason, Hugh S
APPLICANT: Hag, Tarig A.
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/782,832
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
                                                                                                       LENGTH:
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CLASSIFICATION:
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pravel, Hewitt, Kin STREET: 1177 West Loop South,
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                                                                             TOPOLOGY:
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 l Similarity
12; Conserv
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100.0%; larity 100.0%; Conservative 0
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Loop South, 10th Floor
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 Score 62; DB 11
Pred. No. 0.005;
Mismatches
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Pred. No. 0.005;
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                              DB 11;
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; TYPE: PRT ; ORGANISM: Vibrio cholerae US-09-836-433-14
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US-09-836-433-14
Sequence 14, Application US/09836433; GENERAL INFORMATION:
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US-08-817-906-21
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                                                  NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 103
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Best Local :
                                                                                                              APPLICANT: YUKI, YOShikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CCURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FOX, DAVID L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 361
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fox, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements, APPLICANT: and Tariq A. Haq
APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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1301 McKinney, Suite 5100
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7 100.0%; Pr
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Pred. No.
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Best Local Similarity
Matches 12; Conserva
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Best Local Similarity
~~+~hes 12; Conserv?
                                                                                                         RESULT 15
PCT-US99-30747-55
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Sequence 55, Application PC/TUS9930747
GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at CorTITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 22
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09836433 GENERAL INFORMATION:
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SEQ ID NO 20
LENGTH: 116
TYPE: PRT
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
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50 VEVPGSQHIDSQ 61
                                                                                                                                                                  50 VEVPGSQHIDSQ 61
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Pred. No.
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Pred. No. 0.005;
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                                                                                                                                                                                                                                                            Score 62;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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5 US-09-791-537-19387
5 US-09-791-537-38611
5 US-09-791-537-38639
5 US-09-791-537-68591
5 US-09-791-537-684-8
5 US-10-110-364-10
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0 US-09-791-537-9972
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Compugen Ltd.
                 Sequence 19387, A
Sequence 38631, A
Sequence 38631, A
Sequence 68591, A
Sequence 8, Appli
Sequence 10, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 20, Appl
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	16, Appli 11, Appl 16, Appl 18, Appl 21, Appl 21, Appl 23, Appl 131854, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 130348, 14031, 1	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		 Appli 	9, Appli	4, Appli	123948,	7, Appli	5, Appli	129309,	42610, A	 Appli 	130348,	131854,	15, Appl	•	21, App1	•	•	16, Appl	11, Appl	6, Appli

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEO ID NO 38611
; LENGTH: 103
; TYPE: PRT
; ORGANISM: pdb 1CHPD
US-09-791-537-38611
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GENERAL INFORMATION:
GENERAL IN
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; ORGANISM: pdb 1CT1D
US-09-791-537-19387
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US-09-791-537-38611
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US-09-791-537-19387
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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nilarity 100.0%;
Conservative 0;
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Pred. No. 0.00086;
; Mismatches 0;
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RESULT 5
US-09-791-537-74385
US-09-791-537-74385, Application U
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
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US-09-791-537-68591
RESULT 4
US-09-791-537-68591
RESULT 4
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US-09-791-537-38639
; Sequence 38639, Application US/09791537
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US-09-791-537-68591
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US-09-791-537-38639
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SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 68591
LENGTH: 103
TYPE: PRT
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/791,537 CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 103
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Pred. No.
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Pred. No. 0.00086;
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Pred. No.
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RESULT 7
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US-10-110-364-8
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 74385
LENGTH: 103
TYPE: PRT
                                                                                                                                                                                                Sequence 10, Application US/10110364 GENERAL INFORMATION:
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Best Local
APPLICANT: Handley, Harold H.
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERIS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
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TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
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LOCATION: (1)...(103)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 998409
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ORGANISM: Vibrio cholera
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PRIOR FILING DATE: 2000-10-05

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; NAME/KEY: VARIANT; LOCATION: (1)...(103); CTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511 US-10-110-364-10
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; Sequence 22, Application US/10110364
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 103
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           APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
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NUMBER OF SEQ ID NOS: 31
CURRENT APPLICATION NUMBER: US/10/110,364
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LOCATION: (1)...(103)
GOTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235
OTHER INFORMATION: (Ogawa 41 R35D).
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TYPE: PRT
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12; Conserv
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Pred. No.
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Pred. No. 0.00086;
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ORGANISM: Escherichia coli;
FEATURE:
NAME/KEY: VARIANT;
LOCATION: (1)...(103)
CTHER INFORMATION: LTB variant from NCBI gene bank GI: 494265.
US-10-110-364-22
                                                                                                                                                                                              US-09-791-537-99772; Sequence 99772, Application US/09791537; GENERAL INFORMATION: APPLICANT: Bionomix, Inc.
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US-09-791-537-87980
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 99772
LENGTH: 104
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 103
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87980, Application US/09791537
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEC ID NOS: 15305
                                                                                                          APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 104
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                             51 VEVPGSQHIDSQ 62
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104;
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ORGANISM: pdb 3CHBD

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Sequence 12, Application US/10110364

GENERAL INFORMATION:

APPLICANT: Handley, Harold H.

APPLICANT: Hasparanta, Tapio

APPLICANT: Ewalt, Karla L.

TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS

FILE REFERENCE: ACTBIO.004A

CURRENT APPLICATION NUMBER: US/10/110,364

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: PCT/US90/27607

PRIOR APPLICATION NUMBER: 60/158,561

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                       ; ORGANISM: pdb 1LTRD US-09-791-537-73608
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                                                                                                                                                                                  Sequence 73608, Application US/09791537

GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Desceph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
CORTWAREN BEACHTICE.
                                                                                                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 73608
LENGTH: 113
TYPE: PRT
                                   Query Match
Best Local Similarity
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Best Local
                     Matches
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LOCATION: (1)...(105)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa OTHER INFORMATION: 41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 105
TYPE: PRT
ORGANISM: Vibrio cholera
FEATURE:
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51 VEVPGSQHIDSQ 62
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Local Similarity 100.0%;
ses 12; Conservative 0
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ilarity 100.0%;
Conservative 0;
                     Conservative
                                 100.0%; Score 62; DB 5; 100.0%; Pred. No. 0.00096;
                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No. 0.00087;
                   Mismatches
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                                                  Length 113;
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                   Indels
                 0;
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                 Gaps
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                 0;
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US-10-110-364-17
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                                                                                                                             TYPE: PRT
ORGANISM: Escherichia c
FEATURE:
Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 123
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 VEVPGSQHIDSQ 82
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0 VEVPGSQHIDSQ
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Sequence 20, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION UNMERR: US/10/110,364
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                               NAME/KEY: VARIANT
LOCATION: (1)...(123)
OTHER INFORMATION: LTB variant from NCBI gene bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (1)...(123)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1395122
100.0%; Score 62; DB 6; ilarity 100.0%; Pred. No. 0.0011; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 6; Pred. No. 0.0011;
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                                                 Length 123;
     Indels
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Gaps

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Database
                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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62
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                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                               283138 seqs, 96089334 residues
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                                                                                                                                                                                                                                                                                                          1 VEVPGSQHIDSQ 12
                                                             PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                            pir1:*
pir2:*
pir3:*
pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ر ت	4	w	2	1	No.	Result
35	35	35	35	35	35	35	35	36	36	36	36	36	36	37	37	37	37	37	37	37	38	38	39	39	39	40	62	62	Score	
56.5	56.5	56.5	56.5	56.5	56.5	56.5	56.5	58.1	58.1	58.1	58.1	58.1	58.1	59.7	59.7	59.7	59.7	59.7	59.7	59.7	61.3	61.3	62.9	62.9	62.9	64.5	•	100.0	Match:	% Query
371	367	360	313	302	284	259	142	1785	755	455	373	368	368	550	442	423	378	376	367	352	674	282	353	272	260	242	124	124	Length 1	
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		hypothetical prote	protein B0495.8 [i	catechol 1,2-dioxy	methylenetetrahydr	hydrolase вн3805 [cytochrome-c oxida	probable membrane	probable beta-gala	glucarate dehydrat	probable 4-carboxy	histidinol-phospha	histidinol-phospha	hypothetical prote		hypothetical prote	hypothetical prote	chorismate synthas	gibberellin 20-oxi	hypothetical prote	carbon-monoxide de	hippocampus-derive		hypothetical prote	protein F20B17.2 [hypothetical prote	heat-labile entero	cholera enterotoxi	scription	

A;Molecule type: DNA
A;Residues: 1-20, 'Q', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A;Residues: 1-20, 'Q', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A;Reperimental source: classical biotype strain 569B
R;Dams, E, de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A;Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A;Reference number: S1/665; MUID:91355224

A;Cross references: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94613.1; GSPDB:GN:A;Experimental source: serogroup O1; strain N16961; biotype El Tor R;Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J.
Chinese Biochem. J. 9, 395-399, 1993
A;Title: Nucleotide sequence analysis of the gene encoding the classical biotype V.ch A;Reference number: JC1078
A;Accession: JC1078

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833 A;Accession: H82196

A; Molecule type: DNA A; Residues: 1-124 <H

1-124 <HEI>

A; Status: preliminary

ALIGNMENTS

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A;Accession: S17666
A;Molecule type: DNA
A;Residues: 1-38,'H',40-67,'T',69-124 <DA2>
A;Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41591.1; PID:g48890
A;Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41591.1; PID:g48890
A;Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41591.1; PID:g48890
A;Max Q.J.: Liu, C.X.; Xiong, L.S.; Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric: Med. Earth Sci. 34, 274-280, 1991
A;Title: B subunit of cholera toxin produced in Escherichia coli.
A;Reference number: PC1010
A;Accession: PC1010
                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 1
C;Complex: the cholera enterotoxin molecule
ciate noncovalently with the subunit B, an a
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 22-38,'H','40-42,'N','44-67,'T',69-90,'N'
A; Experimental source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to Asp
C; Comment: The authors translated the codon TCA for
                                                                    멍
                                                                                                         Ş
                                                                                                                                                                                                                                                                F;1-21/Domain: signal sequence *status predicted <SIG>F;22-124/Product: cholera enterotoxin chain B *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: DNA
A;Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A;Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A:Cross-references: GB:X00171; NID:g48347; PIE
R:Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A;Title: Covalent structure of the beta chain
A;Reference number: A01819; MUID:78005537
A;Accession: A01819
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A; Residues: 22-30, 'H', 40-41 < MAQ>
R; Mekalanos, J.J.; Swartz, D.J.; Pearson,
Nature 306, 551-557, 1983
A; Reference number: A93320; MUID:84068199
A; Accession: A05130
      RESULT
                                                                                                                                                                                                                                                                                                                C; Keywords: enterotoxin; toxin
                                                                                                                                                                                                                                                                                                                                  C; Superfamily: cholera enterotoxin
                                                                                                                                                                                                                                                                                                                                                    A; Description: involved in binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Takao, T.; Watanabe, H.; Shimonishi, Y.
Eur. J. Biochem. 146, 503-508, 1985
A;Tille: Facile identification of protein
A;Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 22-38, 'H', 40-67, 'T', 69, 'E', 71, 'QS', 74-75, 'VE', 78-86, 'Q', 88-99, 'Q'
R; Takao, T.; Watanabe, H.; Shimonishi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124
A;Note: the difference at residue 70 may be due to deamidation dur
R;Nakashima, Y: Napiorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A38033; MUID:78005536
A;Accession: A38033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: VC1456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124
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                                                                                                                                                         Matches
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                                                                                           1 VEVPGSQHIDSQ 12
                                                                    VEVPGSQHIDSQ
                                                                                                                                                                             Similarity
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                                                                                                                                                                           Score 62;
Pred. No.
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beta chain
                                                                                                                                                      Mismatches
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aggregate
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hes 0;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-17, (C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A;Cross-references: GB:S60731; NID:g408994; PIDN:AAC60441.1; PID:g408996
R;Tsuj1, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.
Microb. Pathog. 2, 381-390, 1987
A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin A;Reference number: A61475; MUID:89180953
A;Accession: A61475
                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124
A; Experimental source: strain 240-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A. FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from A;Reference number: I53542; MUID:93252225
A;Accession: I67644
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C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999
C;Accession: A01820; B26946; I41194; I41287; I67644; A61475
                                                                                                    F;30-107/Disulfide
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A; Molecule type: DNA
A; Residues: 1-5, F', 7-17, 'C', 19-24, 'S', 26-27, 'E', 29-33, 'H', 35-63, 'K', 65-66, 'A', 68-122
A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831
A; Experimental source: plasmid ENT-R PCG86
R; Ibrahimi, I.; Gentz, R.
J. Biol. Chem. 262, 10189-10194, 1987
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A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <YAM>
A; Residues: 1-27, 'E', 29-63; NID:g148335;
A; Cross-references: EMBL:M15363; NID:g148335;
R; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
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Nature 288, 499-501, 1980
A;Title: Amino acid sequence homology between
A:Reference number: A01820; MUID:81074965
                                                                                                                                                      F;1-21/Domain: signal sequence #status predicted
                                                                                                                                                                                                        A;Description: the biological activity of the C;Superfamily: cholera enterotoxin beta chain
                                                                                                                                                                                                                                                                                 C; Complex: the heat-labile enterotoxin molecule contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-22 < RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Yamamoto, T.; Gojobori, T.; Yokota, J. Bacteriol. 169, 1352-1357, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: I41287
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R; Yamamoto, T.;
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                            Query Match
Best Local
  Matches
                                                                                                                                                                                   Keywords: enterotoxin
  . Similarity
12; Conserv
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Conservative
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                                                                                                      bonds: #status
                          100.0%;
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                               Pred.
                                                  Score 62;
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1 VEVPGSQHIDSQ 12

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RESULT 5
T14755
hypothetical protein DKFZp564A0122.1 - human
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change |
C;Accession: T14755
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wieman; submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F20B17.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96B27
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, E.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roy, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: C96B27
A. Accession: C96B27
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A; Gene: SCO
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A; Cross-references: EMBL: AL031184; PIDN: CAA20190.1; GSPDB: GN00070;
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Gene:
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mes 6; Conserv
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                                                                                                                                                                                                                               VKVPGKQHVSEK 76
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                     Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, he Protein Sequence Database, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                50.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                     Length 260
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                                                                                20-Sep-1999
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A;Cross-references: GB:M34643
R;Maisonpierre, P.C.; Belluscio, L.; Squinto, S
science 247, 1446-1451, 1990
A;Title: Neurotrophin-3: a neurotrophic factor
A;Reference number: A40094; MUID:90208301
A;Accession: A40094
                                                                                                                                                                                        hippocampus-derived neurotrophic factor precursor - rat
N;Alternate names: neurotrophin-3 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-oct-1990 #sequence_revision 05-oct-1990 #text_change 16-Jul-1999
C;Accession: A35781; A40094
R;Ernfors, P; Ibanez, C.F.; Ebendal, T.; Olson, L.; Persson, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990
A;Title: Molecular cloning and neurotrophic activities of a protein with sta
A;Reference number: A35781; MUID:90319130
A;Accession: A35781; MUID:90319130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T14755
A; Status: preliminary
A; Moleoule type: mRNA
A; Residues: 1-272 <WAM>
A; Cross-references: EMBL: ALI10209
A; Experimental source: fetal brain; clone DKFZp564A0122
A; Note: DKFZp564A0122.1
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
A35781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
C; Superfamily: (S)-2-hydroxy-acid oxidase;
F; 3-297/Domain: (S)-2-hydroxy-acid oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896 A;Accession: H75446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: (03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-282 <ERN>
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A;Experimental source: strain R1
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A; Residues: 1-353 <WHI>
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Best Local 9
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nes 6; Conserv
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Pred. No.
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                                                                                      S.; Ip, N.Y.; Furth, M.E.;
                                             related
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                                                                                                                                                                                                                                          protein with structural
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T.; Zalewski,
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                                                                                        Lindsay, R.M
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RESULT 9
B85518
hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7, substrain hypothetical protein 20347 [imported] - Escherichia coli (strain 20347 [imported] - Escherichia
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A41670
A41670
Carbon-monoxide dehydrogenase (EC 1.2.99.2) beta chain [similarity] - Clostridium C;Species: Clostridium thermaceticum C;Species: Clostridium thermaceticum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-352 <STO>
A;Residues: 1-352 <STO>
A;Cross-references: GB:AE005174; NID:g12513064; PIDN:AAG54606.1;
A;Cross-imental source: strain O157:H7, substrain EDL933
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C;Superfamily: carbon-monoxide dehydrogenase beta chain; hybrid cluster [4Fe-2S-30] homo
C;Keywords: 4Fe-2S-30; 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; q
F;256-606/Domain: hybrid cluster [4Fe-2S-30] homology <HCL>
F;256-606/Domain: hybrid cluster (4Fe-4S-30] homology <HCL>
F;68,71,76,90/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F;283,321,355,470,500,550,585/Binding site: Ni-3Fe-2S-30 cluster (His, Glu, Cys, Cys, F;470/Modified site: cysteine persulfide (Cys) #status predicted
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A;Title: The primary structure of the subunits of carbon monoxide dehydrogenase/acetyl-A;Reference number: A41670; MUID:92084676
A;Accession: A41670
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A; Residues: 25-282 <MAI>
A; Cross-references: GB: M33968; NID: g205771; PIDN: AAA41727.1; PID: g205772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-352 <S'
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A; Residues: 1-674 < MOR>
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Best Local
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54.5%;
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                                                                                                                                                                                                                         Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB Pred. No. 45;
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                                                                                                                                                                                                                                                       Length 352
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                                                                                                                                                                                       0;
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                                  RESULT 12
F90667
hypothetical
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protein

ECs0310

[imported]

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Escherichia coli (strain

0157:н7,

substrain

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C;Superfamily: chorismate synthase
C;Keywords: phosphorus-oxygen lyase; transmembrane
F;347-363/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterization
A;Reference number: S17246; MUID:92114793
A;Accession: S17246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces W,Alternate names: protein G2501; protein YGL148w C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text C;Accession: S17246; S64162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
C;Superf
                                   δÃ
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-376 <VOL>
A; Cross-references: EMBL: Z72670; NID:g1322731; PIDN:CAA96860.1;
                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence Database, A; Reference number: S64153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gibberellin 20-oxidase - common tobacco
N;Alternate names: Ntcl6 protein
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
C;Accession: T01751
                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                       A; Gene: SGD: ARO2; MIPS: YGL148w
                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S64162
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C;Genetics:
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A; Accession: T01751
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                                                                                                                                                                                                                                       A;Cross-references: SGD:S0003116; MIPS:YGL148w
                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                               A; Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X60190; NID:g3386; PIDN:CAA42745.1; R;Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-376 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Jones, D.G.L.; Reusser, U.; Braus, G.H.
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A; Residues: 1-367 <TAN>
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                                                                          Matches
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7; Conserv
                                                                          Similarity 7; Conser
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87.5%;
                                                                                             70.0%;
                                                                                                                59.7%;
                                                                                                                  Score 37;
                                                                                             Pred. No. 37;
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                                                                          Mismatches
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                                                                                                                  Length 376;
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hypothetical protein F19C24.16 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: 696554
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alactic 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                         zuotin-like protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T39633; T40195
R;Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A:Residues: 1-378 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAB33733.1; PID:g13359767; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RIMD 0509952
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90667
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A; Reference number: Z21869
A; Accession: T39683
A; Status: preliminary; tran
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A; Map position: 1
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C;Genetics:
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A; Residues: 1-423 <STO>
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Best Local S
Matches 6
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;Gene: ECs0310
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Best Local Similarity
Matches 6; Conserv
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Kasunaga, T.; Kuhara, S.;
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    translated from GB/EMBL/DDBJ
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75.0%;
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Shiba, T.; Hattori,
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37;
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A;Residues: 1-124 <OLT>
A;Cross-references: EMBL:AL049489; PIDN:CAB39796.1; GSPDB:GN00067; SPDB:SPBC1778.01c
A;Experimental source: strain 972h-; cosmid c1778
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A submitted to the EMBL Data Library, February 1998
A;Reference number: Z21910
A;Recession: T40195
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 89-442 <WOO>
A;Residues: 89-442 <WOO>
A;Experimental source: strain 972h-; cosmid c30D10
A;Experimental source: strain 972h-; cosmid c30D10
                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein A_IG002P16.9 - Arabidopsis thaliana (species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change C; Accession: T01770 R; Miller, N.; Beck, C.; Kramer, J. submitted to the EMBL Data Library, June 1997 A; Description: The sequence of A. thaliana IG002P16. A; Reference number: Z14421
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-550 <MIL>
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Search completed: October Job time: 12.2459 secs
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A; Introns: 159/
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Result No.

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[5]
SEQUENCE FROM N.A.
GTRAIN-1854 / 0139-BENGAL;
DO V.G.R.F., X
          SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-2046833; PubMed-19952301;
MEDLINE-2046833; PubMed-19952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera enterotoxin, beta CTXB OR TOXB OR VC1456.
Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                  STRAIN=4260B / SEROTYPE 0139;
MEDLINE=94237453; PubMed=8181723;
Lebens M., Holmgren J.;
"Structure and arrangement of the cholera cholerae 0139,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-EL TOR 2125; Dams E., de Wolf M.
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STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
Mekalanos J.J., Swartz D.J., Pear.
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"Nucleotide sequence analysis of the cholerae enterotoxin.";
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P01556; Q9JQ02;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development.";
Nature 306:551-557(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=84061784; PubMed=6315707;
                                                                                                                                                                                                                                                                                                                    Microbiol. Lett. 117:197-202(1994).
                                                                                                                                                                                                (MAY-1994) to the
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                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE-95387394; PubMed-7558472;
Zhang R.G., Westbrook M.L., Westbrook E.
Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salzberg
Fraser C.
                                                                                                                                                                                                                                           between
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-I- FUNCTION: THE BETA CHAIN AGGREGATE
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[7]
                                                                                                                                                                                                                                                                                                                                                                     Merritt
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Merritt E.A., Sar
Hol W.G.J.;
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MEDLINE-78005536; P
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Kurosky A., Markel D.E., Peterson J.W
"Covalent structure of the beta chain
                                                                                                                                                                                                                                                                                                                                                           Hirst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pentasaccharide.
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L; X76391; CAA53976.1; -.
L; ABD04224; AAF94613.1; -
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A05130; A05130.
S14624; S14624.
S14624; S14624.
CHB; O3-DEC-97.
3CHB; 17-AUG-98.
1CHP; 08-MAR-96.
1CHP; 08-MAR-96.
1CHP; 08-MAR-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. -Y
                                                                                                                                                                                                                                                                       (FROM THE SAME PRECURSOR MOLECULE), DISULFIDE BOND, ASSOCIATE NONCOVALE 6 BETA CHAINS.
                                                                                                                                                                                                                                                                                                   BINDING TO CELL MEMBRANES.
SUBUNIT: CONTAINS 3 KINDS OF CHAINS.
                                                                                                              X00171; CAA24996.1;

K01170; AAA27573.1;

D30053; BAA06291.1;

X58786; CAA41593.1;

X76390; CAA53973.1;

X76391; CAA53976.1;
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STRAIN-ISOLATE H74-114;
MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between cistrons from Escherichia coli of human Infect. Immun. 48:73-77(1985).
                                                                                                                                                             ELBH_ECOLI P13811;
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MEDLINE=83114628; PubM
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HELIX
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STRAND
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                Yamamoto T., Tamura T.A., "Overlapping genes in the from Escherichia coli hum
                                                     Infect.
[2]
                                                                                                                                 ELTB OR LTPB.
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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TIGR; VC1456;
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            188:356-359(1982).
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oxin; Signal; 3D-structure; Complete proteome
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                r.A., Yokota T., T:
n the heat-labile of
i human strain.";
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chain precursor (
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STRAIN=ISOLATE H10407;

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ELBP_ECOLI STANDARD;
ID ELBP_ECOLI STANDARD;
AC p32890; p13768; p01557;
AC p32890; R13768; p01557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.";
T Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.; "Amino acid sequence of heat labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of humm H 10407.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matkovic-Calogovic D., Loregian A., D'Acunto
Tossi A., Palu G., Zanotti G.;
"Crystal structure of the B subunit of Escher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comparison of correct amino acid sequences f enterotoxins of Escherichia coli and Vibrio Mol. Microbiol. 15:1165-1167(1995).
                                                                                                                                                                                                                                                                                              PRINTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
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medline=99185101; pubMed=10085117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95349400; PubMed=7623669; Domenighini M., Pizza M., Jobling M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ETEC LT 87;
Germani Y., Desperrier J.M.;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                 Enterotoxin; Signal;
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                                                                                                         VEVPGSQHIDSQ
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                                                                                          VEVPGSQHIDSQ
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MEDLINE-95349400; pubMed=7623669;

MEDLINE-95349400; pubMed=7623669;

Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R

Tidentification of errors among database sequence entries and

comparison of correct amino acid sequences for the heat-labile

enterotoxins of Escherichia coli and Vibrio cholerae.";

Mol. Microbiol. 15:1165-1167(1995).

-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED

THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmi reticulum.";
                                                            This
                                                                                                                                                                                                                                                                                                     MEDLINE=91238966; PubMed=2034287; Sixma T.K., Pronk S.E., Kalk K.H., Witholt B., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                               "Refined structure of Escherichia coli heat-labile close relative of cholera toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ISOLATE PCG86;
MEDLIND-87137303; PubMed-3546273;
MEDLIND-87137303; PubMed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Amino acid sequence homology between coli heat-labile toxin.";
Nature 288:499-501(1980).
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MEDLINE=95349400; PubMed=7623669;
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MEDLINE-81074965; Pu
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                                                                                                                                                                                                                                                                          "Crystal structure of a cholera toxin-related from E. coli.";
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"A functional interaction
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                                                                                                                                                                                                                                                                                                                                                    -RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                               T.K.,
                                                                                                                                                                                                                                                             351:371-377(1991).
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Best Local
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P27989;
01-AUG-1992
01-AUG-1992
Morton T.A., Runquist J.A., Ragsdale S.W., Shanmuga wood H.G., Ljungdahl L.G.; Wood H.G., Ljungdahl L.G.; The primary structure of the subunits of carbon modehydrogenase/acetyl-CoA synthase from Clostridium J. Biol. Chem. 266:23824-23828(1991).
-i- PUNCTION: CAPALYZES THE INTERCONVERSION OF CO A SYNTHESIS OF ACETYL-COENZYME A FROM THE METHYLA
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or send a
                                                     SEQUENCE FROM N.A.
MEDLINE=92084676; Pubmed=1748656;
                                                                                              15-JUL-1999 (Rel. 38, Last annotation update)
Carbon monoxide dehydrogenase beta subunit (EC 1.2.99.2) (CODH).
Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group;
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L; M15363; AAA2479
L; M17101; AAA2397; A01820; QLECB.
; B26946; QLECEB.
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17-AUG-96.
31-JAN-94.
31-JAN-94.
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license@isb-sib.ch).
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P28777;
01-DEC-1992
01-DEC-1992
30-MAY-2000
                                                                                                                                                                                         WEDLINE-97197983; FUDMEUT-VILLE, Riles L., Robben Joet M., Defoor E., Verhasselt P., Riles L., Robben Joet M., Defoor E., Verhasselt P., Riles L., Robben Joet September of a nearly unclonable 22.8 kb segment chromosome VII from Saccharomyces cerevisiae reveals chromosome VII from Saccharomyces cerevisiae reveals chromosome VII from Saccharomyces cerevisiae reveals
              + +
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                                                                                                                                                                                                                                                                                                                                                                                          of the ARO2 gene, cerevisiae.";
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ARO2 OR YGL148W
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Eukaryota; Fungi; Ascomyc
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-!- SUBUNIT: TETRAMER
-!- SIMILARITY: TO R.
                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92114793; PubMed=1837329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C;
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                                                   11, MRE1 genes and six new open reading frames.";
ist 13:177-182(1997).
CATALYTIC ACTIVITY: 5-O-(1-carboxyvinyl)-3-phosphoshikimate
chorismate + phosphate.
COFACTOR: REDUCED FLAVIN.
PARTHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITH
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATE
SUBBURIT: HOMOTETRAMER (BY SIMILARITY).
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COFACTOR:
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Ascomycota; Saccharomycotina;
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R.RUBRUM CARBON MONOXIDE DEHYDROGENASE.
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IRON-SULFUR (BY SIMILARITY).
IRON-SULFUR (BY SIMILARITY);
54BA3D816C25F9FC CRC64;
                 CHORISMATE
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ABL; X60190; C.,
ABL; X99960; CAA682...
EMBL; X99960; CAA96860.1;
PIR; S17246; S17246.
SGD; S0003116; ARO2.

A InterPro; IPR000453; Chorismate_synt,
DR Prossure; PR01264; Chorismate_synt; 1.
PRODOM; PD002941; Chorismate_synt; 1.
PROSSURE; PS00789; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
""SITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
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STRAIN-WSB8 / DEM 3109;
MEDLINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Stewart A.M., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Bvidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
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       Hypothetical SEQUENCE 24
                                                                            EMBL; AE001773; -; NOT_ANNOTATED_CDS TIGR; TM1158.1; -.
                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Unpublished observations (APR-2001).
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       al protein;
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1; Complete proteome.
27773 MW; 1BEF66C1C8BD2700 CRC64;
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Pfam; PF01188; MR_MLE; 1.
Pfam; PF02746; MR_MLE_N; 1.
Lyase; Complete proteome.
SEQUENCE 455 AA; 50782 MW:
                                       BGAL_THEET P77989;
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01-NOV-1995
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P42238;
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EMBL; Z99105; CAB12043.1;
HSSP; P42206; 1BQG.
SubtiList; BG11161; gudD.
                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: FIRST STEP IN GLUCARATE CATABOLISM.
-!- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-glucarate = 5-dehydro-4-deoxy-D-glucarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICTODIOLOGY 141:269-275(1995).
-!- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogawa K.-I., Akagawa E., Nakamura K., Ya
"Determination of a 21548 bp nucleotide
degrees region of the Bacillus subtilis
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Bacillus/Staphylococcus group; Bacillus.
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ucarate dehydratase (EC 4.2.1.40) (GDH) (GlucD).
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Takeuchi T., Shuman M.A., Craix C.S., "Reverse blochemistry: Use of macromolecular protease inhibitors idissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
                                                                                        SEQUENCE FROM N.A. MEDLINE-99432178; PubMed-10500122; Takeuchi T., Shuman M.A., Craik C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09Y5Y6; 09H3S0; Q9HCA3; Q9BS01; Q9HB36;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15 (Tumor associated differentially-expressed gene-15 protein).
ST14 OR PRSS14 OR SNC19 OR TADG15.
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between
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
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                                                                                                                                                                                                   C.Y., Anders J., Johnson M., Sang Q.A., lecular cloning of cDNA for matriptase, tease with trypsin-like activity.";
Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing galactosides.
SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES
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                                                                                                                                                                                                                                                                                                           PubMed=10373424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
; FE011FF517E51DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                Q.A.,
                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                     , Dickson R.B.;
a matrix-degrading serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω,
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                OR LYS AS THE P1 SITE.

11- SUBCELLULAR LOCATION: Type II membrane protein (Proi-
11- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS
11- SIMILARITY: CONTAINS 2 CUB DOWAINS.

11- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Brien T.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Purification and characterization of a complex containing matriptase and a Kunitz-type serine protease inhibitor from human milk.";

J. Biol. Chem. 274:18237-18242(1999).

-i- FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUBSTRATES WITH ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Brien
                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cao J., Fan W., Zheng
"Genomic analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of 
in human prostate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaguchi N., Mitsui
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AF133086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis of a novel human serine protease SNC1 (JUN-2000) to the EMBL/GenBank/DDBJ databases
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W., Zheng S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10373425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96:11054-11061(1999).
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L outstation -
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InterPro; IPR000859; CUB.
InterPro; IPR001314; Chymotrypsin
InterPro; IPR0012172; LDL_recept_A
InterPro; IPR0012173; ITYPSin.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00087; ldl_recept_a; 4.
Pfam; PF00087; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00042; CUB; 2.
SMART; SM00042; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1. SMART; SM00192; LDLa; 3.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1 EMBL; EMBL; EMBL; EMBL; MEROPS; BC005826; AF283256; P00763; 11 AB030036; AF057145; S01.302; IDPO. AAD42765.2; -... AAF00109.1; -... BAB20376.1; -... AAG15395.1; -... AAG15826.1; -... AAG13949.1; -... Chymotrypsin. LDL_recept_A.

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Best Local S
Matches
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Q04952;
01-NOV-1997
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CONFLICT
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01-NOV-1997 (Rel. 35, Last annotation update)
Putative 1,3-beta-glucan synthase component (EC glucan-UDP glucosyltransferase).
YMR306W OR YM9952.88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                          Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-I-CATALYTIC ACTIVITY: UDP-glucose + {(1,3)-beta-D-glucosyl}(N) = UI + {(1,3)-beta-D-glucosyl}(N+1).
-I-SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I-SIMILARITY: STRONG, TO GLS1 AND GLS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacc
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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InterPro; IPR003440; Glucan_synthase.
Pfam; PF02364; Glucan_synthase; 1.
Hypothetical protein; Transmembrane; Transferase;
                                                                                                                                                                                                         STRAIN-S288C
                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor;
                                         EMBL; 249212; CAA89139.1;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                         370
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                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                               S0004923;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        855
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CUB 1.
CUB 2.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (G)
N-LINKED (G)
FEA -> GTR
R -> S (IN )
A -> V (IN )
                                                                                   is not removed.
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Pred. No.
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CHARGE
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(See http://www.isb-sib.ch/announce/
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52;
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Glycosyltransferase
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Best Local
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01-JUL-1993
15-JUL-1999
Catechol 1,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
Plasmid.
METAL
                                                                                                                                                                                                              MEDLINE-91192610; PubMed-2013408;
Kivisaar M., Kasak L., Nurk A.;
"Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheB, of phenol-degrading Pseudomonas sp. strain EST1001.";
Gene 98:15-20(1991).
-I- CATALYITY ACTIVITY: Catechol + O(2) = cis,cis-muconate.
-I- COFACTOR: FERRIC ION.
                           EMBL; M57500; AAC64900.1; -.
PIR; JN0143; JN0143.
PISSP; P00437; 3PCD.
InterPro; IDR000627; Dioxygenase.
Pfam; PF00775; Dioxygenase; 1.
PROSITE; PS00083; INTRADIOL_DIOXYGENAS;
                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                   Plasmid pEST1412
Bacteria; Proteo
                                                                                                                                                                                                                                                                                                                                                                                                  PHEB_PSESP
P31019;
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                   Aromatic
                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE INTRADIOL
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                    hydrocarbons catabolism;
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SEQUENCE
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Q01609; Q911P9;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein PA2218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. STRAIN=ATCC 15692 MEDLINE=93051258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 313 AA;
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Submitted (FEB-1995) to t
-!- SIMILARITY: SOME, TO
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Rhabditidae; Pelode
NCBI_TaxID=6239;
                                                                                 Pseudomonas.
NCBI_TaxID-287;
                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                       PSEAE
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                                                                                                                                                Pseudomonas aeruginosa
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PubMed=1427017;
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                                                                                                                               Pseudomonadaceae;
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RESULT 14
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Best Local
                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-ATCC 22788 / RIB 128;
MEDLINE-95200965; PubMed-7893753;
Fujita Y., Uraga Y., Tchishima E.;
"Molecular cloning and nucleotide sequence melo, from Aspergillus oryzae and express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
SEQUENCE
                                                               Biochim. Biophys. Acta 1261:151-154(1995).
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998
15-JUL-1998
30-MAY-2000
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufnagle W.Q., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                              cells.";
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
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Nature 406:959-964(2000).
-i- SIMILARITY: TO E.COLI YCJY.
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$23861; $23861.
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3 (Rel. 36, Last sequence update)
1 (Rel. 39, Last annotation update)
1 (EC 1.14.18.1) (Monophenol monooxygenase).
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371 AA;
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R -> P (IN REF. 1).
A -> G (IN REF. 1).
W; D7EB0CCAC95A7CF6 CF
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xpression of the
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Matches 6
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SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    Plant Physiol. 108:1293-1294(1995).
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. B73;
MEDLINE=95357417; PubMed=7630946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                       Xu J., Pemberton G.H., Almira E.C., McCarty D.R., Koch K.E.,
"The Ivr 1 gene for invertase in maize.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D37929;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 EYPGTNSVDSQ 370
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nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVPGSQHIDSQ 12
                                                                                                                                                                                             fructofuranoside residues in beta-D-fructofuranosides.
SUBCELLULAR LOCATION: Vacuolar.
SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMOTETRAMER.
PIM: THE N-TERMINAL IS BLOCKED.
SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: ACTIVATED BY ACIDIFYING TREATMENT AT PH 3.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00497; TYROSINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002227; Tyrosinase.
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB Pred. No. 48; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPPER A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Monooxygenase; Copper.
A (BY SIMILARITY).
A (BY SIMILARITY).
A (BY SIMILARITY).
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B (BY SIMILARITY).
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48;
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MBL outstation -
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                                                                SEQUENCE
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                                                                                                                                                                PROSITE; PS00609;
                                                                                                                                                                        Pfam; PF00251;
                                                                                                                                 PROPEP
                                                                                                                                        SIGNAL
                                                                                                                                                        Hydrolase;
                                                                                                                                                                               InterPro; IPR001362; Glyco_hydro_32.
                                                                                                                                                                                      MaizeDB; 86037;
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61
                                        Local
               1 VEVPGSQHIDSQ 12
VTVLASQHVDGQ
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7; Conser
                                                                                                                                               family.
                                                                670
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09; GLYCOSYL_HYDROL_F32;
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BY SIMILARITY.
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                               1;
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Search completed: October 24, 2002, 15:21:01 Job time: 6.72131 secs

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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: sp_bacteria
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Compugen Ltd
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O9401 vibrio phag
O9176 cryza sativ
O9464 cryza sativ
O94657 cryza sativ
O94867 oryza sativ
O94867 oryza sativ
O946582 streptomyce
O31335 bacillus ce
O9128 streptomyce
O9138 streptomyce
O9138 streptomyce
O94k7 arabidopsis
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		hepatitis	Q92xf7 rhizobium m	4	Φ	Q99gt9 heliocoverp	Q9e226 helicoverpa	Q9u0w5 leishmania		Q9xd79 streptomyce	Q9au17 lycopersico	Q96w68 candida alb	Q96w69 candida alb	004636 arabidopsis	Υ.	Q949w1 arabidopsis	Q9c531 arabidopsis	O80418 nicotiana t	014347 schizosacch	018391 drosophila	Q96ht2 homo sapien			Q94i82 oryza sativ	Q91gm2 oryza sativ	Q9y2b3 homo sapien	Q9rvj7 deinococcus	Q9ug04 homo sapien	Q9ma16 arabidopsis

ALIGNMENTS

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RESULT
Q57193
ID Q5
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OSR646 ...
OSR646 ...
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Best Local :
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Pfam; PF01376; Enterotoxin_B; 1.

PRINTS; PR00772; ENTEROTOXINB.

ProDom; PD012805; Enterotoxin_B; 1.

PEODOM; PD012805; Enterotoxin_B; 1.

SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9R646 PRELIMINARY; PRT; 103 AA.
O9R646; PRT; 103 AA.
O19R646; PRT; 103 AA.
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q57193 PRELIMINARY;
Q57193;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiol. Immunol. 39:87-94(1995). HSSP; P01556; 1XTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95303036; PubMed=7783690;
Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision;
NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHOLERA-LIKE ENTEROTOXIN B SUBUNIT
                                                                                                                                                                                                                                                                          50 VEVPGSQHIDSQ 61
                                                                                                                                                                                                                                                                                                                      1 VEVPGSQHIDSQ 12
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12; Conserv
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           Created)
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                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 2;
Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Best Loc
Matches
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01-MAY-2000
01-MAY-2000
01-JUN-2001
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ProDom;
Signal.
SIGNAL
                                                                                          "Cloning and nucleotide sequence analysis of the cassette from Vibrio cholerae KNIH002 isolated in Misalnmurhag Holj1 35:205-210(1999).
EMBL; AF175708; AAD51360.1; -.
HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CLASSICAL STRAIN 569B;
MEDLINE=91355224; PubMed=1883840;
Dams E., De Wolf M., Dierick W.;
"Nucleotide sequence analysis of classical strain 569B.";
               PRINTS; PR00772; ENTEROTOXINB. ProDom; PD012805; Enterotoxin_B;
                                                                                                                                                                                         STRAIN-KNIH002;
Shin H.J., Park Y.C.,
                                                                                                                                                                                                                                                                                                                               CTXB
                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TREMBLRE1 13, Creat 01-MAY-2000 (TREMBLRE1 13, Last 01-JUN-2001 (TREMBLRE1 17, Last CHOLERA ENTEROTOXIN B-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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STRAIN-CLASSICAL BIOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CLASSICAL Shi C., Cao C., 2
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 SEQUENCE
                                                       InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
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Pfam; PF01376; Enterotoxin_B; 1.
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1-JUN-2001
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A00931; CAA00098.1;
P01556; 2CHB.
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12; Conserv
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 AA;
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J. 9:395-399(1993).
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17, Last annotation updat
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CHOLERA TOXIN B PROTEIN
D6BF83FFF7924EA3 CRC64
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Pred. No.
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 23BF83FFF793E5B9
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annotation update)
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 CRC64;
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
HEAT-LABILE ENTEROTOXIN B
LTH B SUBUNIT.
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Q93V32;
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01-NOV-1996
01-JUN-2001
          STRALM=1032 (ENTEROTOXIGENIC);
MEDLINE=95091056; PURMECH-7998417;
Tamura S., Asanuma H., Tomita T.,
Hattori N., Watanabe K., Suzuki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparison of cholera toxin genes (ctxAB) of non-Ol vibri
strains 854 (0139-bengal) and S7 (037) from two outbreaks.
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; D30052; BAA06289.1; -.
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                                                                                SEQUENCE
                                                                                                                   Submitted
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                                                                                                                                                   STRAIN-1032
                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                     Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                          Escherichia
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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12; Conserv
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AA;
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Conservative
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(ENTEROTOXIGENIC);
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13871 MW;
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    B SUBUNIT.

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HYPOTHETICAL 43.6 KDA PROTEIN.
BG:DS01514.3.
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NCBI_TaxID=7227;
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01-DEC-2001
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Marthl C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K., Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Eukaryota; Metazoa; Arthropoda; Diracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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"The entire core region of the ctx-phi (ctx-prophage) in
environmental strain of V. cholerae.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF414369; AAL09682.1;
SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
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EMBL; AB011677; BAA25726.1; -
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RN [2]

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC CAINIERT S.E., Agbayani A., Arcaina T.T., Baxter E., blue, STRAIN=Y, CN BW SP;

RA Celniker S.E., Agbayani A., Chavez C., Chew M., Cissiolka L., Doyle C.m.,

RA Butenhoff C., Champe M., Chavez C., Chew M., Cissiolka L., Doyle C.m.,

RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

RA HOUSTON K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

RA Zieran L.L., Rubin G.M.;

RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

BR FlyBase; FBgn0028907; BG:DS01514.3.

KW Hypothetical protein.

SEQUENCE 395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;

"A SEQUENCE 395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;

"A SEQUENCE 395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;

"A SEQUENCE 395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;
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Best Local :
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Saski C., Henry D., Oates .
"Rice Genomic Sequence.";
"Rice Genomic Sep-2001) to the control of the 
                                                                                                           Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                    Q94HM6 PRELIMINARY; PRT; 1109 AA. Q94HM6; Q1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat putative Transposable Element.
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Guraryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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    SEQUENCE FROM N.A
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                                                                                        NCBI_TaxID=4530;
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Q94EB4;
Q1-DEC-2001
01-DEC-2001
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01-DEC-2001
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Spiegel L., de la Bastide M., Nascimento L., Kirchoff K., King Spiegel L., de la Bastide M., Ball M., Zutavern T., Santos L. Miller B., Vil M.D., Baker J., Bell M., Zutavern T., Santos L. Miller B., Kuit K., Rodriguez S., Cunnius D.M., Balija V., Shal Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;
"Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBA0089D15, from Chromosome 10, complete sequence.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0002B05.";
Submitted (JAN-2001) to the EMBL/GenBa
EMBL; AP003141; BAB63505.1;
SEQUENCE 1352 AA; 154782 MW; DFF26
                                                                                                                                                                                                                                                                                               STRAIN-CV.
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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EMBL; AC078944; AAK9
SEQUENCE 1109 AA;
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L., Preston R., Vil M.D., Baker J., Bell
os L., Miller B., Kuit K., Rodriguez S.,
R., Bahret A., Bal H., O'Shaughnessy A.,
                                        PGSQHIDSQ
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PGSQHIESE
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9 AA; 127116 !
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Last annotation update)
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Pred. No. 21;
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Baker J., Bell M., Zutavern T.,
Rodriguez S., Cunnius D.M., Balija V.,
Shaughnessy A., Dedhia N.,
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tos L.,
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Wing R.A., Yu Y., Soderlund C
Saski C., Henry D., Oates R.,
"Rice Genomic Sequence.";
Submitted (OCT-2001) to the E
EMBL; AC079852; AALZ5171.1;
SEQUENCE 2535 AA; 289895 M
                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
STRAIN-A3(2);
MEDLINE-97000351; PubMed=8843436;
MEDLINE-97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                        the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996). EMBL; AL031184; CAA20190.1; -. InterPro; IPR002502; Amidase_2.
                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2001 (TrEMBLrel. 17,
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01-DEC-2001 (TrEMBLrel. 19, Last sequen)
01-DEC-2001 (TrEMBLrel. 19, Last annota)
PUTATIVE TNP-LIKE TRANSPOSABLE ELEMENT.
                                                                                                             Hypothetical protein. SEQUENCE 242 AA; 2
                                                                                                                                                              Pfam; PF01510; Amidase_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy L., Harris D.; Submitted (AUG-1998)
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NCBI_TaxID=1902;
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J., Barrell
1 (AUG-1998)
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70.0%;
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R., Simmons
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e EMBL/GenBank/DDBJ
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Score 40; DB
Pred. No. 9.3;
1; Mismatches
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                    Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson Lehrach H., Poustka A., Lundeberg J.; The European IMAGE Consortium for integrated Molecular human gene transcripts."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL389957; CAB97531.1; ...
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LLPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
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Pluvinet R., Estivill X.,
Submitted (JUL-2000) to t
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EMBL; Y11217; CAA72103.1; .
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus.
Bactería; Firmicutes;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ATP-DEPENDENT NUCLEASE SUBUNIT A (FRAGMENT).
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                                                                                                                                        SEQUENCE
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NCBI_TaxID=1396;
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Local Similarity
les 6; Conserv
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Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL133210; CAB61584.1; -.
InterPro; IPR002502; Amidase_2.
Pfam; PF01510; Amidase_2.1.
SEQUENCE 201 AA; 22749 MW; B8EF477E06A20468 CRC64
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Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Cerdeno A.M., Parkhill J., I
Submitted (NOV-1999) to the
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Submitted (NOV-1999)
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-	Peptide #1909 enco		Peptide #1903 enco	Peptide #1957 enco	Yeast ubiquitin.	Ubiquitin componen	Human ubiquitin.	۲	4	Yeast ubiquitin.	Human colon cancer	Human immune/haema	Human cancer assoc	Human endometrium	Propionibacterium	Peptide #11673 enc		Human bone marrow	Human brain expres	Protein #8680 enco	Peptide #11244 enc	Human polypeptide	Cholera toxin B/en	Human nervous syst	Human secreted pro	Cholera toxin B/en	Cholera toxin B su	Bovine rotavirus V	Cholera toxin B su	Cholera toxin B/en	ß	lera toxin B	CTP3 epitope of th

ALIGNMENTS

RESULT 1
AAY87462
ID AAY8

AAY87462 standard;

peptide;

21 B

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.

EtxB;

03-JUL-2000

(first entry)

AAY87462;

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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind tiglycolipid receptor {\tt GM-1} -
                                                                Williams NA, Hirst TR;
                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                            Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                07-SEP-1999;
                                                                                                                                                     16-MAR-2000
                                                                                                                                                                         WO200014114-A1.
                                                                                                                                                                                             Vibrio cholerae.
Escherichia coli.
                                                                                    (UYBR-) UNIV BRISTOL.
                                            2000-256943/22.
                                                                                                           98GB-0019484.
                                                                                                                                99WO-GB02970
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not bind the

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RESULT 2
AAY87463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are Cc composed of one A subunit and five identical B subunits. The A subunit cell surfaces. Both Etx and Ctx are Cc composed of one A subunit and five identical B subunits. The A subunit cell sresponsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) Cc facilitate the entry of subunit A into the host cell via the binding and Cc cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the fects of Etx and Ctx, it has been found that certain Cc through GM-1 binding. The peptides of the invention are fragments of the Obeta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as CC normal EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC for treating, preventing and/or modulating a disease associated with an CC immune disorder and/or toxin-induced diarrhoea. Sequences AAX87460-Y87463 cc represent preferred peptides of the invention, AAX87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                           Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                           Disclosure; Page 15;
                                                                       Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind t
                                                                                                                                                       Williams NA,
                                                                                                                                                                                                                     07-SEP-1998;
                                                                                                                                                                                                                                                   07-SEP-1999;
                                                                                                                                                                                                                                                                                   16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                        E. coli heat labile enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                 WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY87463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY87463 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiguitous
                                                                                                                                                                                     (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L
                                                                                                                           2000-256943/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
21; Conser
                                                         receptor GM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
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                                                                                                                                                       Hirst TR;
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A
                                                                                                                                                                                                                    98GB-0019484
                                                                                                                                                                                                                                                    99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                             62pp; English
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Pred. No. 5.1e-11;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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The invention

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peptide fragments

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Escherichia coli heat

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RESULT 3
AAR72545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC labile enterotoxin (Etx) and its closely related homologue, cholera Ct toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are CC composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, except that they do not bind or cross link CC consul EtxB and CtxB subunits, except that they do not bind or cross link CC They may also be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC Therefore, the peptides may be used in the production of a composition CC immune disorder and/or toxin-induced diarrhoea. Sequences Aav87460-Y87463 CC represent preferred peptides of the invention, Aav87460 being CC particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                    Armstrong
Oomen R,
                                                                              other molecules
                                                                                           New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes
                                                                                                                                                                                                                   (CONN-)
AAR72540-R72545 are structurally equivalent B-ADP-ribosylating toxins, pertussis holotoxtin
                                              Disclosure; Fig 5;
                                                                                                                                         WPI; 1995-132623/18.
                                                                                                                                                                                                                                                               24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                         EP646599-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                              23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                            05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP-ribosylating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR72545 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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UNIV ALBERTA.
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                                                                                                                                                                       GD,
Read
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                                                                                                                                                                    Cockle SA,
1 RJ, Stein
                                                                                                                                                                                                                                                               93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                              94EP-0306219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin (verotoxin-1 B-subunit).
                                              54pp; English.
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95.2%;
                                                                                                                                                                                                                                   LTD.
                                                                                                                                                                       Hazes
PE;
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                                                                                                                                                                                      В,
                                                                                                                                                                                      Klein MH,
 B-subunits
in (PT), E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                       Loosmore
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Cholotoxin. The pertussis holotoxin modification process comprises:
C(1) identification of at least one amino acid (aa) residue of the
C(1) identification of at least one amino acid (aa) residue of the
C(2) crystalline holotoxin, in relation to known information of the protein
C(3) crystalline holotoxin, in relation to known information of the protein
C(4) crystalline holotoxin, in relation to known information of the protein
C(5) crystalline holotoxin and crystalline arganism to compare and (3) expressing mutant tox box in a Bordetella organism to compare the modified holotoxin. This method is used for modifying
C(5) crystalline arganism to compare the holotoxin, alters its biological properties.
C(6) Structure. Modifying the holotoxin, alters its biological properties.
C(6) Colotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa)
C(5) which contribute to the toxicity of the holotoxin to produce communoprotective, genetically-detoxified analogues of pertussis
C(5) holotoxin. The present sequence represents an ADP-ribosylating toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local s
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       labile toxin (IT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                            (CONN-)
                                                                                                                                                                                                                        A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline
                                                                                                                                                                                                                                                                                                                                                                    Read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP-ribosylating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999
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                                                                                                                                                                                                                                                                     Example 3; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1994;
24-AUG-1993;
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                                                                                                                                                                                                                                                                                                New method for
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                                                                                                                                                                                                                                                                                                                                                     s RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                                                                            CONNAUGHT LAB
                                                                                                                                                                                                                                                                                                                                                                                              UNIV
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                                                                                                                                                                                                                                                                                                                                                     Stein
Oomen
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                                                                                                                                                                                                                                                                                               producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0292968
93US-0110947
                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0251121
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                                                                                                                                                                                                                                                                                                                                                     RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxin; PT; crystalline pertussis holotoxin; ETA; structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                  41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                verotoxin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                         LTD.
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                                                                                                                                                                                                                                                                     English
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                                                                                                                                                                                                                                                                                                                                                                  SA,
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                  Loosmore
                                                                                                                                                                                                                                                                                               pertussis holotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-09;
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                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 93;
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RESULT 5
AAW95226
ID AAW9
XX AAW9
XX E. (
XX E
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                                            having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by x-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a binding or enzyme activity of the PT. The three-dimensional structure cell binding and adjuvanticity of the PT. The three-dimensional structure coins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Armstrong
Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme; ADP-ribosylation; structural analysis; inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3;
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other resemblance to pertussis holotoxin with the aim of modifying other
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Hazes B,
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ADP-ribosylating toxin; mannose binding protein;
l structure; X-ray crystallography; detoxification;
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95.2%;
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Pred. No. 2e-09;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify of toxicity, cell binding or enzyme activity of PT and modifying
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Hazes B,
                                                                    21-APR-1992
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24-AUG-1993;
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                                                                                                                                                                                                                                                                          35
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Stein P
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93US-0110947.
94US-0251121.
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coll (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin medicaments -
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  (SCRI-) SCRIPPS CLINIC RES
                                                                                                                                                                             WO8502611-A
                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                  Heat-labile
                                                                                                                                                                                                                                                                                                          Network polymer which comprises a series of composite labile toxin (LT)/heat-stable toxin (ST) polypeptide 1
                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera vaccine;
                                              12-DEC-1983;
                                                                                     12-DEC-1984;
                                                                                                                                   20-JUN-1985
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                                                                                                                                                                                                                                                                enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The
                      composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP504.
                                                                                                                           Claim
                                                                                                                                                 New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                      12-DEC-1983;
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                                                                                                                                                                                                                                           (SCRI-) SCRIPPS CLINIC
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                                                                                                                                                                                           1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GXTFQVEVPGSQHIDSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Page 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                          Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                      83US-0559469
                                                                                                                                                                                                                                                                                              84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                    heat-stable toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           of composite E. coli heat-
polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli enterotoxin(s
                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is Ala or Glu, AAP50439-57.
                                                                                      residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Sequence

41

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RESULT 12
AAP93498
ID AAP93
XX
AC AAP93
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AAP30265
                                                                                                                                                           Query Match
Best Local
                                                                                                                                               Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                  The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
     AAP93498;
                                                                                                                                                                                                                          a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                           Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of amino acids 50-75 of the cholera carries an Arg at posns. 67 and 73.
                            AAP93498 standard;
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guyongruaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP95426-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP30265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP30265 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-1982;
                                                                                             ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQK 18
                                                                                                          VEVPGSQHIDSQKKAI 21
                                                                                            VEVPGSQHIDSQKKAI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1983-834645/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GETFQVEVPGSQHIDSQK 26
                                                                                                                                               l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α,
                                                                                                                                                                                                 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raulais D,
                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82FR-0009167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83EP-0401052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy; E.coli infection; enterotoxin
                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                          75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rivaille P,
                            15
                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                          Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88; DB 6;
Pred. No. 1.2e-07;
0; Mismatches 1
                            B
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Siffert 0,
                                                                                                                                        DB 4;
J. 1.7e-06;
O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin
                                                                                                                                                                     Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                              Indels
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                                                                                                                                              Gaps
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                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
망
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                   Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence corresponds to the CTP3 epitope of the Cholera toxin subunit. The DNA sequence encoding this ligates to othersynthetic oligonuclectides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immure.
                           03-MAY-1994;
                                                   02-MAY-1995;
                                                                              09-NOV-1995
                                                                                                      W09529701-A1
                                                                                                                                Vibrio cholerae
                                                                                                                                                                                                                       Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                  13-JUN-1996
                                                                                                                                                                                                                                                                          AAR85125
                                                                                                                                                                                                                                                                                                    AAR85125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant flagellin gene including sequence - for het epitope, and expressed fusion proteins, useful in vaccines of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTP3 epitope of Cholera toxin B subunit; flagellin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTP3
  (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marjarian WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1990
                                                                                                                                                          intestines; antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRAX-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) LEYLAND STANDFORD JUNIOR UNIV.
                                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDSQKKA
                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                 VEVPGSQHIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1989-356496/48.
DB; AAN92414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epitope
                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRAXIS BIOLOGICS INC
                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fig.4B; 137pp;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                           94IL-0109519
                                                    95WO-EP01661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stocker BAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-0190570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89WO-US01932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Cholera toxin B subunit
                                                                                                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                 71.78;
                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                         secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newton
                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMC;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; 1
4.1e-06;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for prodn.
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Gaps

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RESULT 14
AAR76748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FimH;
FimA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85125, covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
     WPI; 1995-275442/36
                                       Hasty DL,
                                                                           (GXBI-)
                                                                                                               27-JAN-1994;
                                                                                                                                                   27-JAN-1995;
                                                                                                                                                                                      03-AUG-1995
                                                                                                                                                                                                                          WO9520657-A1
                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues 50-64 of cholera toxin B subunit and FimH 224-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR76748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1995-403805/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
15; Conserv
                                                                           GX BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
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                                       Klemm P,
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Escherichia col:
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                                       Molin S,
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                                                                                                                                                                                                                                                          "Represents FimH residue
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                                                                                                                                                                                                                                                                                                                                                                                                      "Represents FimH
                                                                                                                                                                                                                                                                                            "Linker peptide"
                                                                                                                                                                                                                                                                                                                              "Cholera
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Pred. No.
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                  Disclosure; Page 15;
                                                                                                                                                                  Williams
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Query Match
Best Local Similarity
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Derivatives of Escherichia coli heat labile enterotoxins useful immunomodulators and for treating diarrhea and which do not binglycolipid receptor {\rm GM-1} -
                                                                                                                                                                                                                                                                                                                                                                                                                         Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulatic adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY87461 standard;
                                                                                                                                                                                                    07-SEP-1998;
                                                                                                                                                                                                                                         07-SEP-1999;
                                                                                                                                                                                                                                                                                 16-MAR-2000
                                                                                                                                                                                                                                                                                                                        WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a fragment of the the plasmid pLPA93 which was used in the production of finH fusion genes comprising the cholera toxin B subunit inserted into the finH gene. This insert shows the inclusion of the B subunit into the FinH protein at position 224-226. The chimeric genes were then opt. further modified by insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ93061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor specific bacterial adhesins - useful for targetting compounds and microbial cells to locations of receptors
                                                                                                                                                           (UYBR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VEVPGSQHIDSQKKA 19
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                                                                                2000-256943/22.
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                                                                                                                        Hirst TR;
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62pp; English

CC The invention relates to peptide fragments of the Escherichia coli heat Clabile enterotoxin (Etx) and its closely related homologue, cholera CC toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are CC composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and Cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC through GM-1 binding. Such as immunomodulation, are not mediated CC through GM-1 binding. Such as immunomodulation are fragments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC Therefore, the peptides may be used in the production of a composition CC control disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 CC represent preferred peptides of the invention, AAY87460 being CC particularly preferred.

Sequence 12 AA;

Query Match Best Local S Matches Local Similarity 100. ses 12; Conservative 58.5%; Score 62; 100.0%; Pred. No. tive 0; Mismatc Mismatches DB 21; L . 0.00075; ches 0; Length 12; Indels 0; Gaps 0

밁 Ş 1 VEVPGSQHIDSQ 12 6 VEVPGSQHIDSQ 17

Search completed: October 24, 2002, 15:35:04 Job time: 34.7049 secs

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5: /cgn2_6/ptodata/1,
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US-08-26-24-24-2
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US-08-46-34-6
US-08-48-101
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	5, Appl:	23, App.		-	23, App.	•	Appl.	3, App	53, App	•	-	•	l, App	61, App.	6, Appl	16, App	. 5208144	ייקערי

ALIGNMENTS

Application US/08292968

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Sequence 26
Patent No.
GENERAL IN
                                                 TELLEFAX: (416) 595-1163
TRECEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/292,968
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
                                                                                                                                                  FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION UNBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
THE EDUCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MODIFICATION NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim & STREET: Suite 70: CITY: TORONTO STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                TYPE: amino acid
STRANDEDNESS: sir
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TOPOLOGY:
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Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARMSTRONG, Glen D.
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                            Matches
                                                      Query Match
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Patent No. 5965385
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Best Local :
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                                                                                                                                                                         TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: APPLICATION NUMBER: US 08/110,947
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OURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467 CT

FILING DATE:

CLASSITYTE
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-UN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                           Local
                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Suite CITY: Toronto
                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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1 GATFQVEVPGSQHIDSQKKAI 21
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                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 95.:
20; Conservative
                                                                                                                                                                                                                                                                 STEWART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ontario
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                                                                                                                                              93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
Suite 701, 330 University Avenue
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KLEIN, Michel H.
ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAZES, Bart
                                                                                                     linear
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                                                                                                                                                                                                                                                           Michael
                                                                                                                single
                                          95.3%;
95.2%;
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95.2%;
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                            0
                                                                                                                                                                                                                                 1038-454 MIS:vg
                                        Score 101; DB 2;
Pred. No. 1.7e-10;
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Pred. No. 1.7e-10;
                            Mismatches
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                                                      DB 2; Length 93;
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                            Indels
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US-08-467-976-26
                    RESULT 4
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US-08-467-536-26
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US-08-467-536-26
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                                                                                                                                                      Query Match
Best Local
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APPLICATION NUMBER: US 08/292,968

FILING DATE: 22-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION UNUMBER: US 08/251,121

FILING DATE: 31-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I.

NAME: STEWART, Michael I.

NAME: DATA: 24 973
                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                      LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                     35
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     1 GATFQVEVPGSQHIDSQKKAI 21
                                                                     GETFQVEVPGSQHIDSQKKAI
                                                                                                                                      . Similarity 20; Conserv
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Suite 701, 330 University Avenue
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VENTION: MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                      Conservative
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                                                                                                                                                                                                                        linear
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06-JUN-1995
                                                                                                                                                      95.3%;
95.2%;
                                                                     55
                                                                                                                                      0;
                                                                                                                                                      Score 101; DB 2;
Pred. No. 1.7e-10;
                                                                                                                                      Mismatches
                                                                                                                                                                    Length 93;
                                                                                                                                        Indels
                                                                                                                                      0;
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Sequence 26, Application US/08467976 Patent No. 6018022 GENERAL INFORMATION:

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APPLICANT:

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                                                                                                                                                      Sequence 26
Patent No.
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/251,121
                                                                                                                         GENERAL INFORMATION:
APPLICANT: READ, Randy J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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             APPLICANT: ARMSTRONG, GAPPLICANT: HAZES, Bart
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                                                                              APPLICANT:
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NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 24-AUG-1993
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                                                                                                                                                                                                                                                     35 GETFQVEVPGSQHIDSQKKAI 55
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OF SEQUENCES:
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M5G 1R7
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                                                                                                                                                                        Application US/09082514
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                                        STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
ARMSTRONG, Glen D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 MODIFICATION OF PERTUSSIS
46
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95.2%;
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                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                               Score 101;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                Mismatches
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..7e-10;
                                                                                                                                                                                                                                                                                                                                            Length 93;
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US-08-350-884-35
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/08350884 Patent No. 5585258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/680,296
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-AUG-1994 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 24-AUG-1994
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
APPLICATION NUMBER: US 0 FILING DATE: 04-APR-1991
                                                             APPLICATION NUMBER: US/08/350,884 FILING DATE: 06-DEC-1994
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/082,514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                94304-1018
                                                                                                                                                                                                                                            Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                             California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 amino acids
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95.2%;
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Pred. No. 1.7e-10;
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                                                                                                              Version
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                                                                  TOPOLOGY: US-08-709-173-35
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US-08-709-173-35
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   Query Match 34.9
Best Local Similarity 42.9
Matches 9; Conservative
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APPLICANT: HOUGHT
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                           NAME: CIOTTI, THOMAS E.
REGISATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,173
FILING DATE: 06-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HERATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 22: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
                                                                                                                                                                             TELEY: (415) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 42.98;
es 9; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                 linear
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                  34.98;
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5:
 Score 37; DB 1; Length 75; Pred. No. 21; Indels
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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US-08-709-177-35
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                                                                                     GENERAL INFORMATION:
APPLICANT: HOUGHTO
APPLICANT: CHOO, QI
APPLICANT: HAN, JA
                                                                                                                                                  Sequence 3, Application US/08833678A Patent No. 5989905
                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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Patent No.
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                      APPLICANT: CHOO, QUI-LIM
APPLICANT: HAN, JANG
APPLICANT: CHOE, JOONO
TITLE OF INVENTION: HCV NS3 PROTEIN FRAGMENTS HAVING
TITLE OF INVENTION: HELICASE ACTIVITY AND IMPROVED SOLUBILITY
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
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TELEFAX: 706141
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nes 9; Conserv
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REGISTRATION NUMBER: 21,013
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STATE: California
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                                                                                                                       HOUGHTON, MICHAEL
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CHIRON CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                            Pred.
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                                                                                                                                                                                                                                                                                                                              No.
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Intellectual Property - R440, P.O. Box 8097

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US-08-529-169A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,169A
FILING DATE: 15-SEP-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3274
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HCV NS3 PROTEIN FRAGMENTS HAVING TITLE OF INVENTION: HELICASE ACTIVITY AND IMPROVED SOLUBILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-SEP-1995
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FILING DATE: 15-SEP-1995
CLASSIFICATION: 4325
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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Local Similarity 42.9%;
nes 9; Conservative
                                                                                                                                                                                                                    STATE: California
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 94662-8097
                                                                                                                                                                                                                                         CITY: Emeryville
                                                                                                                                                                                                                                                        ADDRESSEE: CHIRON CORPORATION STREET: Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                     CHOO, QUI-LIM
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                                                                                                                                                                                                                                                                                                                                                                        CHOE, JOONHO
                                                                                                                                                                                                                                                                                                                                                                                                                             HOUGHTON, MICHAEL
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linear
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Pred. No.
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10 GKTITLEVESSDTIDNVKSKI 30

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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-232-815-2
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Best Local Similarity '
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US-08-232-815-2
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Patent No. 5503977
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                              TELEFAX: 207 363-0528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 75 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Johnsson, Nils
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: SPLIT UBIQUITIN PROTEIN SENSOR
                                                                                                                                                                        TELEPHONE:
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                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: York Harbor
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Farrell, Kevin M.
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P.O. Box 999
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Conservative
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               34.9%;
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42.98;
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               Score 37; DB Pred. No. 21;
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   Mismatches
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                           DB 1; Length 76
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US-08-468-274-2
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US-08-350-906-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Johnsson, Nils
APPLICANT: Varshavsky, Alexander
APPLICANT: TOTAL TOTAL
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: CIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207 363-0528
TELEFAX: 207 363-0528
                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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STATE: WI
FILING DATE: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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CITY: York Harbor
                                                                    APPLICATION NUMBER: US/08/468,274
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P.O. Box 999
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                                                                                                                                                                                                                                                                                                                                                    USA
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N: 435
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Anti-Viral Mushroom Extracts
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Query Match
Best Local Similarity
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Query Match
Best Local Similarity
Matches 9; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 207 363-0558
TELEFAX: 207 363-0528
                                                                                                                                                                                                                                                                                             CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/350,906
                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
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HYPOTHETICAL: 1
                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                          TOPOLOGY:
                                                                                                                                                                                                               NAME: Farrell, Kevin M. REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-DECCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GKTITLEVESSDTIDNVKSKI 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seay, Nicholas J
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California Institute of Technology
VENTION: UBIQUITIN-BASED SPLIT PROTEIN SENSOR
                                                                                            linear
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               34.9%;
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              Score 37;
Pred. No.
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          , DB 5;
21;
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0,

Conservative

Mismatches

10;

Indels

0

Gaps

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,632

FILING DATE: 19-MAR-1998

CLASSIFICATION NUMBER: US 60/041,016

FILING DATE: 19-MAR-1997

APPLICATION NUMBER: US 60/041,016

FILING DATE: 19-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: COTIESS, Peter F.

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 48147/1699-CIP

TELEPHONE: 617-523-3400

TELEPHONE: 617-523-6440

INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acids

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-045-632-83

14.0%: Score 36; DB 3; Le
                                                                                                              Qy
                                                                                                                                     Query Match
Best Local Similarity
Thehes 7; Conserve
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Search completed: October 24, 2002, 15:38:24 Job time: 14.0492 secs
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US-09-045-632-83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Huganir, Richard L.
APPLICANT: Huganir, Richard L.
APPLICANT: Dong, Hualing
TITLE OF INVENTION: THERAPEUTIC USES OF GRIP AND
TITLE OF INVENTION: GRIP-RELATED MOLECULES
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATFQVEVPGSQHIDSQKKAI 21
| | | | | | | | | |
10 GKTITLEVESSDTIDNVKSKI 30
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ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                            N
                                                                                                  6 VEVPGSQHIDSQKKA 20
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VDVPHASAVDALKKA 16
                                                                                                                                                       Conservative
                                                                                                                                                                         34.08; 46.78;
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                                                                                                                                                                       Score 36; DB 3; Pred. No. 8.8;
                                                                                                                                                       Mismatches
                                                                                                                                                       4; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                Score
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Match
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: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
1: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_COMB.pep:*
/cgn2_6/ptodata/1/paa/US080_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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 1 US-09-786-648-4

1 US-09-786-648-5

    US-08-110-947-10

    US-08-110-947A-26

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    US-08-2732-371A-1

1 US-08-732-371A-1
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ALIGNMENTS

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LOCATION: 45...65; OTHER INFORMATION: OTHER INFORMATION: US-09-786-648-4
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                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
FULE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                             Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 4
LENGTH: 21
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: E. coli
FEATURE:
1 GATFQVEVPGSQHIDSQKKAI 21
                                         Conservative
                                                                                                                                           isolated or synthetic EtxB human variant E. coli
                                       100.0%; Score 106; DB 21; 100.0%; Pred. No. 1.3e-10; o. Mismatches 0;
                                                                                                                                                              beta4-alpha2 loop
                                         Indels
                                                                            Length
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US-09-786-648-5
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US-09-786-648-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR PILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038-303 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEIN, Penélope E
APPLICANT: COCKLE, Stephen A
APPLICANT: OOMEN, Raymond P
APPLICANT: KLEIN, Michel H
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 21
                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: READ, Randy J
                                                                                                                                                                                                                                                                                                  CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Shoemaker and Mattare, STREET: Suite 1203 Crystal Plaza 1 STREET: Davis Hwy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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20; Conserv
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95.2%;
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Pred. No. 9.
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                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                 I, 2001 Jefferson
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US-08-110-947A-26
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                                                                                                                    US-08-110-947A-26
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                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
TELEFAX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                        Query Match
Best Local Similarity
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/08110947A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 89-9456 LUKPAT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEF
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/01
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: READ, Randy J
APPLICANT: STEIN, Penelope E
APPLICANT: COCKLE, Stephen A
APPLICANT: COMEN, Raymond P
APPLICANT: KLEIN, Michel H
                                                                                                                                STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, L. STREET: Suite 1203 Crystal Plaza I, STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
35 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
                1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                        LENGTH:
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                                                                                                                                                          H: 93 amino acids
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                                                          Conservative
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95.2%;
                                                                      95.3%;
95.2%;
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                                                                        Score 101; DB 5;
Pred. No. 6.2e-09;
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                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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                                                                                  Length 93;
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                                                          Indels
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RESULT 5 US-08-251-121-26

Sequence 26, Application US/08251121

GENERAL INFORMATION:

READ, Randy J.

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                                                                                                                                                                     Sequence 1, Application US/08732371
GENERAL INFORMATION:
APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: INFECTING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & McBurney
                                                                                                                                       NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OTTY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/251,121 FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
                                  COUNTRY: UZIP: 20004
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                                                                                                                      ADDRESSEE:
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                                                                D.C
                                                                                                 E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
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                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEIN, Penelope E. COCKLE, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.3%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 6;
Pred. No. 6.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local Similarity
"~+~hes 15; Conserva
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                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,371A
FILING DATE: 09-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UDMBER: IL 109519
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
PRIOR PARTICIN NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08732371A GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109519
EILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 415
STREET: Washington
CITY: Washington
STATE: D.C.
                              REFERENCE/DOCKET NUMBER: MII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VACCINES FOR ORAL TITLE OF INVENTION: INFECTING AGENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARKS, Robert S. SELA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIRELMAN, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No.
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                                                                                                                               MIRELMAN=3
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SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids

amino acid

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; FEATURE:
    NAME/KEY: SITE
    LOCATION: (9)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-463-761
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 761
                                                                                                                                                                                                                                                                                                                                   Sequence 761, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Applicat GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
FULE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT APPLICATION NUMBER: PCT/GB99/02970
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/180,628 PRIOR FILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/758,463
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: E.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 50...61.
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable OTHER INFORMATION: human variant E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino TOPOLOGY: li
                                                                                  ORGANISM: Homo sapiens
                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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Pred. No.
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hes 0;
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0.0022;
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US-09-708-427-6862
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SOFTWARE: FASTSEQ for
SEQ ID NO 4087
LENGTH: 84
TYPE: PRT
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                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6862
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4087, Application US/60188162
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6862, Application US/09708427 GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLOC
                                                                        Query Match
Best Local Similarity
                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/188,162
CURRENT FILING DATE: 2000-05-09
                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..91
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..91
                                                                                                                                   OTHER INFORMATION: Ceres Seq. ID 1816431
                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                           LENGTH: 9:
TYPE: PRT
58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GTTFQVGAGSSEGEDSEGKAI 94
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                 GATFQVEVPGSQHIDSQKKAI
GKTFNLEVKGSEIIQQVKNMI
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                                                          Conservative
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                                                                        41.5%;
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53.3%;
 78
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Pred. No.
                                                                        Score 44; DB
Pred. No. 35;
                                                             Mismatches
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18;
                                                                                       21;
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                                                                                       Length 91
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RESULT 12 US-09-866-066-35

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PCT-US01-01334-5166
; Sequence S166, Application PC/TUS0101334
; GENERAL INFORMATION:
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Best Local Similarity
Watches 7; Conserve
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PRIOR APPLICATION NUMBER: 60/207,152
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,257
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,119
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
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TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00229.US1
CURRENT APPLICATION NUMBER: US/09/866,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benjamin, APPLICANT: Roberds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US01/01334 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC010PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Human Genome Sciences, Inc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 51
TYPE: PRT
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            OR FILING DATE: 2000-07-14
OR APPLICATION NUMBER: 60/225,757
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/226,868
OR FILING DATE: 2000-08-22
OR APPLICATION NUMBER: 60/216,647
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/225,267
OR APPLICATION NUMBER: 60/225,267
OR APPLICATION NUMBER: 60/216,880
OR APPLICATION NUMBER: 60/216,880
OR FILING DATE: 2000-07-07
OR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/220,963 FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-07-11 APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/217,487 FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/214,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/180,628 FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/179,065 FILING DATE: 2000-01-31
                                                                                                                                                                                                                        APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/217,496
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Gotow, Lisa
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Pred. No.
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37;
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                                                                                                                      PRIOR PRIOR
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R APPLICATION NUMBER: 60/231,413
R FILING DATE: 2000-09-08
PR APPLICATION NUMBER: 60/229,509
R FILING DATE: 2000-09-05
R APPLICATION NUMBER: 60/236,367
R APPLICATION UMBER: 60/236,367
                                  APPLICATION NUMBER: 60/240,960 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/239,935 FILING DATE: 2000-10-13
                                                                                                                   APPLICATION NUMBER: 60/237,040 FILING DATE: 2000-10-02
                                                                                                                                                                                APPLICATION NUMBER: 60/236,802 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287
FILING DATE: 2000-09-01
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
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APPLICATION NUMBER: 60/228,924
                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/236,370 FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/237,038
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/237,039 FILING DATE: 2000-10-02
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FILING DATE: 2000-09-25
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                                                                                                                                                                FILING DATE:
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2000-10-13
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OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/232,400

OR FILING DATE: 2000-09-14

OR APPLICATION NUMBER: 60/231,242

OR FILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/232,081

OR FILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/232,080

OR APPLICATION NUMBER: 60/231,414

OR APPLICATION NUMBER: 60/231,414

OR FILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/231,414

OR FILING DATE: 2000-09-08
DR APPLICATION NUMBER: 60/233,064
DR FILING DATE: 2000-09-14
DR APPLICATION NUMBER: 60/233,063
DR FILING DATE: 2000-09-14
DR APPLICATION NUMBER: 60/232,397
DR FILING DATE: 2000-09-14
DR APPLICATION NUMBER: 60/232,399
DR FILING DATE: 2000-09-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR APPLICATION NUMBER: 60/249,215
BR FILING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,264
RR FILING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,214
RR FILING DATE: 2000-11-17
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DR FILLING DATE: 2000-11-17
DR APPLICATION NUMBER: 60/249,207
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OR APPLICATION NUMBER: 60/249,218
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OR APPLICATION NUMBER: 60/249,208
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,213
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APPLICATION NUMBER: 60/230,438
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/215,135
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FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/235,836
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APPLICATION NUMBER: 60/225,759
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/226,681
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FILING DATE: 2000-11-08
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RESULT 14
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OR FILING DATE: 2000-07-26
OR APPLICATION NUMBER: 60/21
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OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/22
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OR APPLICATION NUMBER: 60/22
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OR APPLICATION NUMBER: 60/21
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OR FILLING DATE: 2000-02-04
OR APPLICATION NUMBER: 60/214,886
OR FILLING DATE: 2000-06-28
OR APPLICATION NUMBER: 60/217,487
OR FILING DATE: 2000-07-11
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OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,826
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,786
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,221
OR APPLICATION NUMBER: 60/241,221
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R APPLICATION NUMBER: 60/2-8
R FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/2:
R FILING DATE: 2000-09-08
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APPLICATION 1
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APPLICATION |
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FILING DATE: 2000-09-14
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NUMBER: 60/225,757
                                            NUMBER:
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             60/234,274
                                            60/235,834
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PRIOR APPLICATION NUMBER: 60/240,960 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/239,935 PRIOR FILING DATE: 2000-10-13 PRIOR FILING DATE: 2000-10-13 PRIOR APPLICATION NUMBER: 60/239,937 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/246,474 PRIOR FILING DATE: 2000-11-08 PRIOR APPLICATION NUMBER: 60/246,532 PRIOR PILING DATE: 2000-11-18	APPLICATION NUMBER: 60/229, 3 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, 3 FILING DATE: 2000-09-25 APPLICATION NUMBER: 60/229, 3 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, 3 FILING DATE: 2000-09-01 APPLICATION NUMBER: 60/229, 2 FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/229, 5 FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/231, 4 FILING DATE: 2000-09-05 FILING DATE: 2000-09-05 FILING DATE: 2000-09-05 FILING DATE: 2000-09-05 APPLICATION NUMBER: 60/236, 3 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237, 0 FILING DATE: 2000-10-02	PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: 60/224,518 PRIOR APPLICATION NUMBER: 60/224,518 PRIOR APPLICATION NUMBER: 60/234,518 PRIOR APPLICATION NUMBER: 60/234,519 PRIOR FILING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/220,964 PRIOR FILING DATE: 2000-09-29 PRIOR PRILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/241,809 PRIOR APPLICATION NUMBER: 60/244,299 PRIOR APPLICATION NUMBER: 60/245,327 PRIOR APPLICATION NUMBER: 60/236,327 PRIOR APPLICATION NUMBER: 60/236,327 PRIOR PILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/236,327 PRIOR PILING DATE: 2000-10-20 PRIOR PILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR APPLICATION NUMBER: 60/25,268 PRIOR PILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 60/25,268 PRIOR PILING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/25,368 PRIOR FILING DATE: 2000-11-08 PRIOR APPLICATION NUMBER: 60/251,856 PRIOR PILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: 60/251,856 PRIOR PILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: 60/251,868 PRIOR PILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: 60/251,856 PRIOR PILING DATE: 2000-12-08 PRIOR APPLICATION NUMBER: 60/251,868 PRIOR PILING DATE: 2000-12-08
PRIOR FILLING DATE: 2000-09-14 PRIOR APPLICATION NUMBER: 60/233,063 PRIOR APPLICATION NUMBER: 60/232,397 PRIOR APPLICATION NUMBER: 60/232,397 PRIOR FILLING DATE: 2000-09-14 PRIOR FILLING DATE: 2000-09-14 PRIOR APPLICATION NUMBER: 60/232,399 PRIOR APPLICATION NUMBER: 60/232,401 PRIOR APPLICATION NUMBER: 60/232,401 PRIOR APPLICATION NUMBER: 60/241,808 PRIOR APPLICATION NUMBER: 60/241,808 PRIOR FILLING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/241,786	PRIOR EFILING DATE: 2000-11-17 PRIOR EFILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,245 PRIOR APPLICATION NUMBER: 60/249,245 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR FILLING DATE: 2000-11-17 PRIOR PRIOR APPLICATION NUMBER: 60/249,211 PRIOR APPLICATION NUMBER: 60/249,211 PRIOR APPLICATION NUMBER: 60/249,211 PRIOR APPLICATION NUMBER: 60/249,215 PRIOR APPLICATION NUMBER: 60/249,215 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,216 PRIOR APPLICATION NUMBER: 60/249,217 PRIOR APPLICATION NUMBER: 60/249,297 PRIOR APPLICATION NUMBER: 60/232,400 PRIOR APPLICATION NUMBER: 60/232,400 PRIOR APPLICATION NUMBER: 60/232,080 PRIOR APPLICATION NUMBER: 60/231,244 PRIOR FILLING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/249,210 PRIOR FILING DATE: 2000-11-17 PRIOR PRIOR APPLICATION NUMBER: 60/226,681 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,759 PRIOR APPLICATION NUMBER: 60/225,213 PRIOR PRIOR APPLICATION NUMBER: 60/227,182 PRIOR APPLICATION NUMBER: 60/227,182 PRIOR APPLICATION NUMBER: 60/225,214 PRIOR APPLICATION NUMBER: 60/235,836 PRIOR FILLING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: 60/235,836 PRIOR APPLICATION NUMBER: 60/235,438 PRIOR APPLICATION NUMBER: 60/235,438 PRIOR APPLICATION NUMBER: 60/245,236 PRIOR APPLICATION NUMBER: 60/249,218

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RESULT 15
US-60-143-993-1325
US-60-143-993-1325
Sequence 1325, Application US/60143993
GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: HEREOF
FILE OF INVENTION UNDEER: US/60/143,993
CURRENT APPLICATION NUMBER: US/60/143,993
CURRENT APPLICATION NUMBER: US/60/143,993
CURRENT FILING DATE: 1999-07-15
SOFTWARE: FastSEQ for Windows Version 3.0.
SEQ ID NO 1325
LENGTH: 44
TYPE: PAT
ORGANISM: Drosophila
US-60-143-993-1325
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Search completed: October 24, 2002, 15:45:17 Job time: 141.77 secs
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PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,398
PRIOR APPLICATION NUMBER: 60/232,398
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Best Local Similarity 50.0%;
Matches 11; Conservative
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11 GAVLQTEISGEQH 23
                                                                                                              1 GATFQVEVP-GSQHIDSQKKAI 21
                                                                                       4 GADQRIEVPVGVQVYDDQQKLI 25
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| Cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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                  US-10-219-999-51216
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US-10-182-995-28451
US-10-203-134-37782
US-10-203-136-37757
US-10-203-135-36160
US-10-203-135-36160
US-10-203-135-36373
US-10-203-139-36373
US-09-791-537-137751
US-09-350-401A-3183
US-09-791-537-120702
US-09-791-537-120702
US-09-791-537-120704
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US-09-620-393B-3233
US-09-791-537-81337
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12211, A
812451, A
817782, A
817787, A
816005, A
816005, A
817905, A
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3, Appli
81370, A
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137751,
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Best Local
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US-10-203-135-35581	US-10-182-998-13901	us-10-182-997-25812	US-10-182-997-22308	US-10-182-993-36014	US-10-182-993-29373	US-10-203-136-37062	US-10-203-136-29998	US-10-203-134-37031	US-10-203-134-29975	US-10-182-995-27979	US-10-182-995-23617	US-09-791-537-74565	US-10-203-139-30215	US-10-203-138-15288	US-10-203-135-30068	US-10-182-998-14849	US-10-219-999-59647	US-10-203-138-12274
Sequence 3	Sequence 1	Sequence 2	Sequence 2	Sequence 3	Sequence 2	Sequence 3	Sequence 2	Sequence 3	Sequence 2	Sequence 2	Sequence 2	Sequence 7	Sequence 3	Sequence 1	Sequence 3	Sequence 1	Sequence 5	Sequence 1
35581,	13901,	25812,	22308,	36014,	29373,	37062,	29998,	37031,	29975,	27979,	23617,	74565,	30215,	15288,	30068,	14849,	59647,	12274,
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ALIGNMENTS

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Sequence 761, Application US/10217607
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PM011C1N
CURRENT APPLICATION NUMBER: US/10/217,607
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 09/758,463
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 761
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-09-620-393B-3233
; Sequence 3233, Application US/09620393B
; General information:
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1068P
CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT APPLICATION NUMBER: US/09/620,393B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature ; LOCATION: (9) CTHER INFORMATION: Xaa equals any of the naturally occurring US-10-217-607-761
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 52.4 nes 11; Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            US-10-219-999-51216
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US-09-791-537-81337
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SEQ ID NO 51216
LENGTH: 60
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                                                    APPLICANT: Stein, Joshua
TITLE OF INVENTION: CONA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILLE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, M
APPLICANT: Hinkle, Gre
                                      NUMBER OF SEQ ID NOS: 63520
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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LOCATION: 1..84
OTHER_INFORMATION: Xaa is any amino acid
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LOCATION: 1..84
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Hinkle, Gregory J.
Kovalic, David K.
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Pred. No. 27;
4; Mismatches
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Pred. No. 14;
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 30 June 2000 (30.06.00)
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Best Local Similarity
Fighther 5; Conserve
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LENGTH: 87
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Best Local
PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 29119

SOFTWARE: Molecular Dynamics Sequence Listing Engine
EQ ID NO 28451
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
FILE REFERENCE: PB 0004 WO 1
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APPLICANT: Lutfiyya, Linda L.
APPLICANT: MCIDINCH, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-08-02
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CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
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RESULT 8
US-10-203-136-37757
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 37782 LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: US 24263.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PB 0004 WO 6
CURRENT APPLICATION NUMBER: US/10/203,134
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 51
TYPE: PRT
                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: EXPRESSED IN BONE MARROW,
                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: MAP TO AL109658.5
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
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OTHER INFORMATION: MAP TO AL109658.5
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                                                                               DLPGKSHLISKKK 35
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Pred. No.
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
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LENGTH: 51
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                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/182,993
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.03
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
FILE REFERENCE: PB 0004 WO 2
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PRIOR FILLING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILLING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/668,408
PRIOR APPLICATION NUMBER: US 09/668,408
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PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: EST_HUMAN HIT: AV651727.1,
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Hanzel, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10182993
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharron G.
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46.2%;
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Pred. No.
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     (27.09.00)
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; OTHER INFORMATION: EST_HUMAN HIT: AV651727.1, EVALUE 4.00e-15 US-10-182-997-26224
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US-10-182-997-26224
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    Best Loc
Matches
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 26941

SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 26224

LENGTH: 51

TYPE: PRT
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 06 February 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 03 October 2000 (03.10.00) PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PB 0004 WO 10
CURRENT APPLICATION NUMBER: US/10/182,997
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Molecular Dynamics, Inc. APPLICANT: Penn, Sharron G.
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PRIOR FILING DATE: 21 September 2000 (2)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: MAP TO AL109658.
                                                                                                                               FEATURE
                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                       Local Similarity
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Chen, Wensheng
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Rank, David
    Conservative
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                                                                                                                                                                                                                                                                                                                                          30 June 2000 (30.06.00)
)S: 26941
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                                                                                                                                                EXPRESSED IN HELA, SIGNAL -
                                                                                                                                                                                           MAP TO AL109658.5
                     35.8%;
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46.2%;
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                     Score 38; Pred. No.
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Pred. No.
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 06 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 OCTOBET 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 60/268,408
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 37905, Application US/10203137
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Matches 6; Conserv
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LENGTH: 51
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                                                                                                                                                                                                                 APPLICANT: Molecular Dynamics, APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
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                                                  CURRENT APPLICATION NUMBER: US/10/203,137
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                             APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILE REFERENCE: PB 0004 WO 7
  PRIOR FILING DATE: PRIOR APPLICATION 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Molecular Dynamics Sequence Listing Engine
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
FILE REFERENCE: PB 0004 WO 5
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OTHER INFORMATION: MAP TO AL109658.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: EST_HUMAN HIT: AV651727.1,
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: 04 February 2000 (04.02.00)
NUMBER: US 60/207,456
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46.2%;
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Pred. No. 56;
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PRIOR FILING DATE:

26 May

2000 (26.05.00)

APPLICATION NUMBER: US 09/632,366
FILING DATE: 03 August 2000 (03.08
APPLICATION NUMBER: GB 24283.6

(03.08.00)

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US-10-203-139-36373; Application US/10203139; GENERAL INFORMATION:
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; OTHER INFORMATION: EST_HUMAN HIT: AV651727.1, EVALUE 4.00e-15
US-10-203-137-37905
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR PRIOR DATE: 04 February 2000 (04.02.00)
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 03 OCTOBER 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/234,369
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
                                                                                                                PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 37156
SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 36373
LENGTH: 51
TYPE: PRT
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NUMBER OF SEQ ID NOS: 38837

SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 37905

LENGTH: 51

TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
FILE REFERENCE: PB 0004 W0 4
CURRENT EPPLICATION NUMBER: US/10/203,139
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Molecular Dynamics, Inc.
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PRIOR FILING DATE: 27 September 2000 (27.09.00)
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FEATURE:
OTHER INFORMATION: EXPRESSED IN FETAL LIVER,
                                             FEATURE:
OTHER INFORMATION: MAP TO AL109658.5
                                                                                                ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/234,687
FILING DATE: 21 September 2000 (21.09.00)
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Rank, David R.
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46.2%;
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Pred. No.
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US-09-350-401A-3025
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                                                                                                                                                                         APPLICANT: HOWARD M. Grey
APPLICANT: ROBERT CHESNUT
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RE
TITLE OF INVENTION: HEPARITIS B VIRUS USING PE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 2060.0060008
CURRENT APPLICATION NUMBER: US/09/350,401A
CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
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SEQ ID NO 137751
LENGTH: 76
TYPE: PRT
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Best Local
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Matches 6; Conserv
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APPLICANT:
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CURRENT FAPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT:
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-07-04
                                                                   PRIOR APPLICATION NUMBER: US 08/205,713 PRIOR FILING DATE: 1994-03-04
                                                                                                       PRIOR APPLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
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Maria A. Vitiello
Brian D. Livingston
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Ralph T. Kubo
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Pred. No. 90;
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SEQID NO 3025

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Artificially Synthesized Peptide

US-09-350-401A-3025

Query Match
Best Local Similarity 61.5%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TFQVEVPGSOHID 15

QY 3 TFQVEVPGSOHID 15

Db 3 SFGVEPSGSGHID 15

Search completed: October 24, 2002, 15:47:34

Job time: 45.7869 secs
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Title:
Perfect score:
Sequence:
                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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106
1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                       283138 seqs, 96089334 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	₅	4	ω	2	_	Result No.
32	32	32	32	32	32	32	32	33	33	34	34	34	35	36	36	36	36	36	36	36	36	36	36	38	40	40	41	44	Score
30.2	30.2	0	0	30.2	0	30.2	0	31.1	31.1	32.1	32.1	32.1	•	34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0	35.8	37.7	7.	38.7	41.5	Query
79	78	78	77	77	63	38	35	95	70	80	70	70	77	99	99	98	88	82	77	77	76	76	41	79	79	79	91	91	Length
N	Ν	Н	N	ب	N	N	N	N	N	N	N	2	N	N	Ν	Ν	ب	2	2	N	N	ш	N	N	N	N	2	2	DB
S77831	D81025	UQUTC	S77465	TUQUT	T43808	F60657	T02997	T14743	D75413	F87520	AI2538	I39058	G81388	S62680	S12161	S28243	YSQU	D75321	S16263	S19799	S12114	UQOA	T36863	в98034	н95167	C95152	F81109	C96580	ID
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ALIGNMENTS

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RESULT 3

C95.152
IS66 family element, Orfl [imported] - Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; bate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change
C; Accession: C95152
C; Accession: C95152
                                                                                                                                                          R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, nson, T.; Hickey, E.K.; Holt, I.E.
                                                                                                                                                                                                                        1366 family element, Orf1 (imported) - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Decies: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change C;Accession: H95167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005672; PIDN:AAK75412.1; A;Experimental source: strain TIGR4 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE002469; GB:AE002098; NID:g7226446; PIDN:AAF41600.1; PID:g7226 A;Experimental source: serogroup B, strain MC58 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mor.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrean Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556 A;Accession: F81907
                                                                                               Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.;
A;Title: Complete Genome Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
  A; Molecule
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A; Residues: 1-79
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A; Residues: 1-91 < PAR>
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                                                                              ng, F.; Smith, H.O.; Venter, quence of a virulent isolate MUID:21357209; PMID:11463916
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Pred. No.
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A, strain Z2491
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21;
                                                                                                                                                                                 Eisen, J.A.;
S.L.; Lewis,
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                                                                                                 J.C.;
of St
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                                                                                                                                                                                 Read,
M.R.;
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                                                                                                   Streptococcus
                                                                                                                      Dougherty,
                                                                                                                                                                               T.D.; Peterson, S.; Hei
Radune, D.; Holtzapple,
                                                                                                                                                                                                                                               03-Aug-2001
                                                                                                                                                                                                                                                                                     (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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A; Title: Genome of the Bacterium Streptococcus pneumoniae Str. A; Reference number: A97872; MUID:21429245; PMID:11544234
A; A; A; Cession: B98034
A; Status: preliminary
A; Molecule type: NNn
A; Pononiae type: NNn
                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
T36863
                                                                                                                          A; Experimental source: C; Genetics: A; Gene: SCOEDB: SCI5.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degenerate transposase (orf1) [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: B98034
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; De
                                                                                                                                                                                                                                                                                                      probable two-component sensor kinase - Streptomyces coelicolor (fragment) C;Species: Streptomyces coelicolor C;Deecies: Streptomyces coelicolor C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 03-Dec:1999 C;Accession: T36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE007317; PIDN:AAL00103.1; PID:g15458942; GSPDB:GN00174 C;Genetics: A;Gene: IS1381-truncation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005672; PIDN:AAK75537.1; PID:gl4972931; GSPDB:GN00164; TIGR: A;Experimental source: strain TIGR4 C;Genetics: A;Gene: SP1443
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-41 <SEE>
A; Cross-references: EM
                                                                                                                                                                                                                                                                          R;Seeger, K.; Harris, D.; Bentley, S.D.; submitted to the EMBL Data Library, June
                                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                          A; Reference number: A; Accession: T36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-79 <KUR>
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Best Local S
Matches
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Best Local
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Best Local
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                            GATFQVEVPG 10
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7; Conserv
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                                                                             Similarity
                                                              Conservative
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                                                                                                                                                          EMBL:AL079332; PIDN:CAB45294.1; ce: strain A3(2)
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40
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Pred. No. 21;
4; Mismatches
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Pred. No. 45;
4; Mismatches
                                                                           Score 36;
Pred. No.
                                                                                                                                                                                                                            from
                                                                Mismatches
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1999
                                                                           48;
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E.J.; Lu, J.; Matsushima,
                                                                                            2
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ubiquitin - oat
c;Species: Avena sativa (oat)
c;Species: Avena sativa (oat)
c;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 16-Aug-1996
C;Accession: A02576
R;Vierstra, R,D.; Langan, S.M.; Schaller, G.E.
Biochemistry 25, 3105-3108, 1986
A;Title: Complete amino acid sequence of ubiquitin from the higher plant Avena sativa.
A;Reference number: A02576
A;Accession: A02576
A;Accession: A02576
A;Residues: 1-76 <VIE>
c;Superfamily: ubiquitin; ubiquitin homology
c;Keywords: protein degradation
F;1-76/Domain: ubiquitin homology <UBH>
F;76/Cross-link: isopeptide carboxyl end (Gly) (interchain to Lys N6-amino of other protein
                                                                                                                                                                    ubiquitin - potato

c;Speciles: Solanum tuberosum (potato)

C;Date: 30-Jun-1992 #sequence_revision

C;Accession: S19799; S19801; S19800

R;Belknap, W.
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$12114
$12114

cylorinus congregatus) (fragment)

cyspecies: Coprinus congregatus

cyspecies: Coprinus congregatus

cyspecies: 21-Nov-1993 #sequence_revision 17-Jul-1998 #text_change 23-Jul-1999

cysccession: $12114
                                                                                                                               R;Belknap, W.
submitted to the EMBL Data Library, January 1992
A;Reference number: S19798
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A;Cross-references: EMBL:Z11672; NID:g21607; PIDN:CAA77738.1; PID:g21608
                   A; Molecule type: mRNA
A; Residues: 1-48 <BEL2>
                                                   A;Cross-references: EMBL:Z11671; NID:g21603; A;Accession: S19801
                                                                                    A; Molecule type: mRNA
A; Residues: 1-56 <BEL1>
                                                                                                                      A; Accession: S19799
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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92;
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                                                                   PIDN:CAA77737.1; PID:g21604
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mating type
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A;Cross-references: EMBL:X56601; NID:g21899; C;Superfamily: ubiquitin; ubiquitin homology C;Keywords: polyprotein F;1-76/Product: ubiquitin *status predicted F;1-76/Domain: ubiquitin homology <UBH>
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S16263
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A; Molecule type: mRNA
A; Residues: 37-77 <BELS>
A; Cross-references: EMBL:Z11673; NID:g21605; PIDN:CAA77739.1; PID:g21606
C; Superfamily: ubiquitin; ubiquitin homology
C; Keywords: protein degradation
E; 1-76/Domain: ubiquitin homology <UBI>
                                                                                                                                                                                                                                                                                                                                           ribosomal protein L33 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Wheat ubiquitin gene exhibits a conserved A;Reference number: S16263; MUID:91316227 A;Accession: S16263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S16263
R; Joshi, C.P.; Weng,
Plant Mol. Biol. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquitin precursor - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
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Best Local Similarity
"---hes 9; Conserv?
                                                                                                                                                                                                   A;Reference number: A75250; MUID:20036896
A;Accession: D75321
A;Stature
                                                                                                                                                                                                                                                       R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
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Best Local Similarity
---has 9; Conserv
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                                                              A; Map position:
C; Superfamily: I
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A; Residues: 1-77 <JOS>
                                                                                                A;Gene:
                                                                                                                           A; Experimental source:
                                                                                                                                              A; Cross-references:
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-82 <WHI>
                                                                                                                                                                                              A;Status: preliminary
                                                                                                              Genetics
 Matches
             Query Match
Best Local
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                                                                                                DR2049
 Similarity
10; Conserv
                                                              Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 Conservative
                                                                                                                               GB:AE002041;
ce: strain R1

    wheat (fragment)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Nguyen, H.T.
907-908, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
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                                                                                                                                            GB:AE000513;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36;
Pred. No.
2;
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                Score 36; DB 2;
Pred. No. 1e+02;
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 Mismatches
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93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA39938.1; PID:g21900
                                                                                                                                              NID:g6459838; PIDN:AAF11599.1; PID:g645
                                                                                                                                                                                                                                               bacterium Deinococcus
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 7;
                              Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 77;
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T.; Zalewski,
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GATFQVEVPGSQHIDSQKKAI

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polyubiquitin - large-leaved lupine (fragment) (;Species: Lupinus polyphyllus (large-leaved lupine) (;Species: Lupinus polyphyllus (large-leaved lupine) (;Date: 21-Nov-1993 #sequence_revision 17-Jul-1998 #text_change 23-Jul-1999 (;Accession: S12161 R;Perrey, R.; Warskulat, U.; Wink, M. Nucleic Acids Res. 18, 6428, 1990 Nucleic Acids Res. 18, 6428, 1990 A;Title: Molecular cloning of a cDNA for the ubiquitin gene of Lupinus polyphyllus. A;Reference number: S12161; MOID:91057134
                                                                                                                                                                                                                                            RESULT
S12161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X13251
C;Superfamily: ubiquitin; ubiquitin homology
C:Keywords: polyprotein; protein degradation
F;1-11/Product: ubiquitin (fragment) #status
F;12-87/Product: ubiquitin #status predicted
F;12-87/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Walker, J.E.; Arizmendi, J.M.; Dupurs, A. J. Mol. Biol. 226, 1051-1072, 1992
A;Title: Sequences of 20 subunits of NADH: A;Reference number: S28237; MUID:92389317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B12 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 02-Dec1933 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999 C;Accession: S28243
A; Molecule type:
A; Residues: 1-99
                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-98 <WAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fortin, M.G.; Purohit, S.K.; Verma, D.P. Nucleic Acids Res. 16, 11377, 1988
A;Title: The primary structure of soybean A;Reference number: S02222; MUID:89083578
A;Accession: S02222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ubiquitin precursor - soybean (fragment)
N;Alternate names: polyubiquitin
C;Species: Glycine max (soybean)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X63213; NID:g235; PIDN:CAA44898.1; PID:g236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S28243
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A; Residues: 1-88 <FOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1;
Pred. No. 1.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2;
Pred. No. 1.2e+02;
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Search completed: October Job time: 17.8361 secs

24,

2002,

15:37:45

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R;Redkar, R.J.; Lemke, P.A.; Singh, N.K.
Curr. Genet. 29, 130-135, 1996
A;Title: Isolation of differentially expressed cDNA clones
A;Reference number: S62677; MUID:96418874
A;Accession: S62680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: protein degradation
C; Superfamily: ubiquitin; ubiquitin; protein degradation
C; Keywords: nucleus; polyprotein; protein degradation
F;1-22/Product: ubiquitin (fragment) *status predicte
F;1-22/Domain: ubiquitin homology (fragment) <UBHI>
                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-99 < RED>
C; Superfamily: ubiquitin
F; 1-76/Domain: ubiquitin
                                                                                                                                                                                                                                                                                                                              ubiquitin/ribosomal protein S27a fusion protein - Emw C;Species: Emericella nidulans, Aspergillus nidulans C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #: C;Accession: S62680
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                                ρ
                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown;
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F;23-98/Domain: ubiquitin homology <UBH2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X54381; NID: g19513; PIDN: CAA38256.1; PID: g19514
                                                                                          Query Match
Best Local
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10 GKTITLEVESSDTIDNVKTKI
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Pred. No. 1.
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                                                                                                       Length 99;
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                                                                        Indels
                                                                                                                                                                 ribosomal
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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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106
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  SwissProt_40:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
    GenCore version (c) 1993 - 2002
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UBIQ_YEAST
UBIQ_YEAST
UBIQ_SOYBN
NB2M_BOVIN
UBIQ_ACACA
UBIQ_PHYIN
                                                                                                                                                                                                                                   TYBO_TORMA
UBIO_ACECL
UBIO_AGLNE
UBIO_CAEEL
UBIO_CHLRE
UBIO_TRYBB
                                       UBIQ_TRYCR
ACP_SYNY3
PTHP_BACME
Y121_CHLPN
FERN_NOSMU
Z600_DROME
YEHE_ECOLI
FER_MASLA
YSDA_ECOLI
UBIQ_EUPEU
UBIQ_EITA
UBIQ_EUPEU
UBIQ_EITA
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Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                 P08618 dictyosteli
P13117 neurospora
P04838 saccharomyc
P19848 coprinus co
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Q02365
Q023634
P225834
P22589
Q91980
Q91980
Q91980
P42740
P14792
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P14624
 P49635
P23398
Q50663
P50715
Q64263
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P20804
Q69250
Q92960
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P002469
P033344
P00248
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glycine max
bos taurus
canthamoeb
phytophthor
cyprinus ca
torpedo mar
acetabulari
aclanthamni
caenorhabdi
chlamydomon
trypanosoma
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coprinus co
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MEDLINE-87257921; PubMed=3037345; Giorda R., Ennis H.L.; Giorda R., Ennis H.L.; Giorda R., Ennis H.L.; Structure of two developmentally regulated Dictyostelium discoideum ubiquitin genes."; MOJ. Cell. Biol. 7:2097-2103(1987). [4] MOJ. Cell. Biol. 7:2097-2103(1987). [4] STRAIN-AX2; Westphal M., Mueller-Taubenberg A., Noegel A., Gerisch G.; "Transcript regulation and carboxyterminal extension of ubiquitin in Dictyostelium discoideum."; FEBS Lett. 209:92-96(1986). -i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME -i- FUNCTION: Unclear and Cytoplasmic. -i- MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN FUECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.	um discoideum (% Mycetozoa; Dicty 44689; OM N.A. OM N.A. Estation of identific il and id	RESULT 1 UBIQ_DICDI UBIQ_DICDI STANDARD; PRT; 76 AA. ID 018618; BT 01-AUG-1988 (Rel. 08, Created) DT 01-AUG-1988 (Rel. 08, Last sequence update) DT 01-KOV-1991 (Rel. 20, Last annotation update)

send

an email to

license@isb-sib.ch).

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UBIQ.WEDGE

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01-JAN-1990
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VARIANT
                STRAIN=ST. LAWRENCE 74 / SL 74 / MEDILINE=91323720; Pubmed=1650731; MEDILINE=91323720; Pottewold E., Aise Taccioli G.E. Grotewold E., Aise The cDNA sequence and expression
                                                                                                                                     Taccioli G.E., Grotewold E., Aisemberg G.O., "Ubiquitin expression in Neurospora crassa: a polyubiquitin gene.";
Nucleic Acids Res. 17:6153-6165(1989).
                                                                                                                                                                                                                        STRAIN-ST. LAWRENCE 74 / SL 74 / MEDLINE-89366647; PubMed-2549509;
                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Neu
NCBI_TaxID=5141;
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PROSITE; PS00299; UBIQUITIN_1;
PROSITE; PS50053; UBIQUITIN_2;
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DictyDb; DD05001; u
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InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
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M19666; AAA33259.1; AI

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L; M19492; AAA33250.1; AI

L; M23749; AAA33253.1; AI

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L; M23751; AAA33256.1; AI

L; M23752; AAA33266.1; AI

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9; Conserv
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Neurospora.
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                                     Aisemberg G.O., Judewicz D.N.;
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CONJUGATION TO ACCEPTOR PROTEINS.
K -> N (IN SOME CLONES REPEATS).
6427383968EABAB4 CRC64;
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Pred. No. 5
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13-AUG-1987
01-MAR-2002
Ubiquitin.
                                                 Saccharomyces Carting (Yeast), and Candida albicans (Yeast), and Cryptococcus neoformans (Filobasidiella neoformans). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomyces
                                                                                                 (UBI1 OR RPL40A OR YIL148W) AND (UBI2 OR RPL40B of UBI3 OR RPS31 OR YIR167W OR L9470.14) AND (UBI4 Saccharomyces cerevisiae (Baker's yeast), Candida albicans (Yeast), and
                                                                                                                                                                                                                     UBIQ_YE:
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A. SPECIES=S.cerevisiae;
                                        Saccharomycetales;
NCBI_TaxID=4932, 5
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EMBL; U01220; AAA56880.1; ALT_TERM.
EMBL; U01221; AAA03351.1; ALT_TERM.
PIR; S05323; UQNC.
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MEDLINE=94374698; PubMed=8088539;
Tarawneh K.A., Anumula K.R., Free S.J.;
"The isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
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SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
MISCELLANGOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH 4 EXACT HEAD TO TAIL REPEATS. THERE IS A FINAL
AMINO-ACID (GLN) AFTER THE LAST REPEAT. SOME UBIQUITIN GENES
CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
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                                                                                                                                                                                                                                    YEAST
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SM00213; UBQ; 1.
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                                           Saccharomycetaceae;
176, 5207;
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42.9%;
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Pred. No. 17;
3; Mismatches
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CONJUGATION TO ACCEPTOR PROTEINS
994480FE7D38403E CRC64;
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MEDLINE=85061630; PubMed=6095120;

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SEQUENCE FROM N.A. (UBI1).

SPECIES=S.cerevisiae; STRAIN=S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser

Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (UBI3).

SPECIES-S. cerevisiae; STRAIN=S288C / AB972;
SPECIES-S. cerevisiae; STRAIN=S288C / Cooper J., Ding H., I
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., I
Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnston L., Langston Y., Latrelile P., Le T.,
Johnston D., Johnston L., Langston Y., Latrelile P., Le T.,
Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Pelus
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S cerevisiae;
MEDLINS=94205265; Pubmed=8154186;
Bou G., Esteban P.F., Baladron V.,
Remacha M., Jimenez A., del Rey F.,
"The complete sequence of a 15,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87275838; PubMed-3038523;
Oezkaynak E., Finley D., Solomon M.J., Varshavsky A.;
Oezkaynak E., Finley D., Solomon M.J., Varshavsky A.;
"The yeast ubiquitin genes: a family of natural gene fusions.";
EMBO J. 6:1429-1439(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[2]
SPECIES=S.cerevisiae;
MEDLINE=95166210; Pub
                                                                          "A proteolytic signal.";
                                                                                     SPECIES=S. Cerevisiae;
MEDLINE=95340540; PubMed=7615550;
Johnson E.S., Ma P.C.M., Ota M., Varshavsky A.;
TA proteolytic pathway that recognizes ubiquitin
                                                                                                                                                                                                 "Structure of the ubiquitin-encoding neoformans.";
                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=C.albicans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                            MEDLINE=95369720; PubMed=7642124;
Spitzer E.D., Spitzer S.G.;
                                                                                                                                                                                                                                                                                                           Submitted
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9:1349-1354(1993).
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                                                             Chem.
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(SEP-1995) to t
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                                                                                                                                                                                                                                                                                                                                       albicans;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .cerevisiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOV-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                          270:17442-17456(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frames.";
                                                                                                                                                                                                                                                                                                                                       (UBI1).
; STRAIN=ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                 (UBI4).
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                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                    Brown A.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V., Gonzalez G.A., Cantalejo J.(
y F., Ballesta J.P.G., Revuelta,
y F., Bayent of Saccharomyces
ins the UBI2 and MPL1 genes and
                                                                                                                                                                                                                                                                                                                                        26555;
                                                                                                                                                     GLY-76
                                                                                                                                                                                                               genes of Cryptococcus
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Spence J.,
"A ubiquit
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MOI. Cell. Biol. 15:1265-1273(1995).

-I FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION

-I CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE

REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSC

BIOGENESIS AND DNA REPAIR.
                       use by non-profit institutions as long modified and this statement is not removed
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entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquitin mutant with
                                                                                                                                                                       PROTEIN.

MISCELLANEOUS: IN S.CEREVISIAE UBI4 IS A POLYPROTEIN CONTAININ EXACT HEAD TO TAIL REPEATS OF UBIQUITIN, THERE IS A FINAL AMINO-ACID (ASN) AFTER THE LAST REPEAT.

MISCELLANEOUS: IN C.ALBICANS UBI4 IS A POLYPROTEIN CONTAINING EXACT HEAD TO TAIL REPEATS OF UBIQUITIN, THERE IS A FINAL AMINO-ACID (PHE) AFTER THE LAST REPEAT.
                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the El European Bioinformatics Institute. There are no rest:
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
MISCELLANEOUS: UBII AND UBII ARE SYNTHESIZED AS A POLYPROTEIN WITH ONE COPY OF UBIOGOMAL PROTEIN S37. UBI3 IS A POLYPROTEIN WITH ONE COPY OF UBIQUITIN FUSED TO ANOTHER RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sadis S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haas A.L., Finley D.;
with specific defects in
                                                       as its content
                       Usage
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tities requires a license agreement (S send an email to license@isb-sib.ch). (See http://www.isb-sib.ch/announce/ a collaboration outstation commercia

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EMBL; U3262/; AAA82979.
EMBL; U16992; AAA82979.
PIR; A22696; UQBY.
                                                            BINDING
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                        PIR;
PIR;
PIR;
                                                                                                                                                                                                  InterPro; IPR000626; Ubiquitin. pfam; pF00240; ubiquitin; 1. pRINTS; pR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                               PIR;
PIR;
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EMBL;
EMBL;
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                                                                                                                          SITE
                                                                                                                                                                                                                                                                           HSSP; P02248; 1UBI.
SWISS-2DPAGE; P04838; YEAST.
SGD; S0001410; RPL40A.
SGD; S0001802; RPL40B.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                   MUTAGEN
                                                                                                                                                                           PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2;
           MUTAGEN
                                                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                L; Z54197; CAA90901.1, Z54197; CAA90901.1, Z54197; CAA86130.1; Z36059; CAA86130.1; Z36057; AAA84000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; X01473; CAA25704.1; Z
X01474; CAA25706.1; Z
X05728; CAA29195.1; Z
X05729; CAA29196.1; Z
X05729; CAA29197.1; Z
X05730; CAA29197.1; Z
X05731; CAA29198.1; Z
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D29456; D29456.
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A29456; A29456.
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Z28319; CAA82173.
U17246; AAB67466.
                                                                                                                                                   protein;
29
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29
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                                                                                                                                                  Polyprotein;
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                      INVOLVED IN UB-UB LINKAGES OF MULT:
UBLOUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS.
K->R: DEFICIENCY IN UBIQUITIN-PROTI
CONJUGATE FORMATION.
K->R: DEFICIENCY IN UBIQUITIN-PROTI
CONJUGATE FORMATION.
                                                                                                                        INVOLVED IN UB-UB LI UBIQUITIN ADDUCTS.
K->R: DEFICIENCY
CONJUGATE FORMATI
                                                                                                             UBIQUITIN ADDUCTS
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LINKAGES OF
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UBIQUITIN-PROTEIN
LOSS OF DNA REPAI
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RESULT 5
UBIQ_SOYBN
ID UBIQ_SOBORC P03993
                                                                                                                                                                                                                                                           RESULT
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Best Local
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P19848;
01-FEB-1991
01-FEB-1991
15-DEC-1998
                                                                                                                                                                                                                                                           BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Basidio
Agaricales; Coprinaceae;
NCBI_TaxID-5347;
     UBIQ_SOYBN P03993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coprinus congregatus.";
Nucleic Acids Res. 18:6449-6449(1990).
-I- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-CALIFORNIA; MEDLINE-91057153; PubMed-2173831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _copco
                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00299; UBIQUITIN_1; 1. PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel form of ubiquiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coprinus congregatus (Inky cap fungus)
                                                                                                                                                                                                                                                                                                                                  Nuclear
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                                                                                                                GKTITLEVESSDTIDNVKAKI 30
                                                                                                                                                GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; X54672; CAA38483.1;
S12114; S12114.
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                                                                                                                                                                                                                                                                                                                                                                                     SM00213; UBQ;
                                                                                                                                                                                      Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                               protein;
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9; Conserv
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6 AA;
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                                                                                                                                                                                                                                                                                                              Polyprotein; Multigene family.
                                                                                                                                                                                                                                                         76
8541 MW;
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                                                                                                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                                                                                       NECESSARY FOR BRÂNCHED-CHAIN MULTIUBIQUITIN ADDUCTS. CONJUGATION TO ACCEPTOR PROTEINS. 852936397D384O3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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35;
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   PPPRE ROUND SONT TO THE PROPRE PROPRE
                                                                                                                                                                                                                                                                                                                                                                  Watts F.Z., Moore A.L.;
Watts F.Z., Moore A.L.;
"Nucleotide sequence of a full length cDNA clone
polyubiquitin gene from Pisum sativum.";
Nucleic Acids Res. 17:10100-10100(1989).
             SEQUENCE FROM N.A. (UBQ1; UBQ2; UBQ5 AND UBQ6).
SPECIES-A.thaliana; STRAIN-CV. COLUMBIA;
MEDLINE-90324239; PubMed-2165066;
Callis J., Raasch J.A., Vierstra R.D.;
"Ubiquitin extension proteins of Arabidopsis thaliana."
                                                                                                                          Burke T.J., Callis J., Vierstra R.D.; "Characterization of a polyubiquitin gene Mol. Gen. Genet. 213:435-443(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1986
23-OCT-1986
15-DEC-1998
                                                                                                                                                                                MEDLINE=89039731; PubMed=2460733;
                                                                                                                                                                                                   SPECIES-A.thaliana;
                                                                                                                                                                                                                    SEQUENCE FROM N.A. (UBQ4).
                                                                                                                                                                                                                                                       Avena sativa.
Biochemistry
                                                                                                                                                                                                                                                                                                            SPECIES=A.sativa;
Vierstra R.D., Langan
                                                                                                                                                                                                                                                                                                                               SPECIES=A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=P.sativum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89033578; pubMed-2849766; Fortin M.G., Purohit S.K., Verma D.P.S.; The primary structure of soybean (Glycine identical to other plant ubiquitins."; Nucleic Acids Res. 16:11377-11377(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. NCBI_TaxID=3847, 3888, 4498, 4499, 4513, 4565, 4577, 4232, 3702, 3870, 3874, 4081, 4113, 4006, 4096, 4686, 4530, 4043, 51350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica rapa (Turnip).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linum usitatissimum (Flax) (Linseed),
Nicotiana sylvestris (Wood tobacco),
Asparagus officinalis (Garden asparagus),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helianthus annuus (Common sunflower),
Arabidopsis thaliana (Mouse-ear cress),
Lupinus albus (White lupine),
Lupinus polyphyllus (Large-leaved lupine),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (F
Triticum aestivum
Zea mays (Maize),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avena sativa (Oat),
Avena fatua,
                                                                                                                                                                                                                                                                                         "Complete amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94211917; PubMed=8159798;
Bao-Sen X., Waterhouse R.N., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petroselinum crispum (Parsley) (Petroselinum hortense),
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SPECIES=Soybean;
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SPECIES-H.annuus; STRAIN-C...

MEDLINE-89183614; PubMed-2538802;

MEDLINE-89184614; PubMed-2538802;

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MEDLINE-89184614; PubMed-2538802;

MEDLINE-89184614; PubMed-2538802;

MEDLINE-89184614; PubMed-2538802;

MEDLI
               Jacinto A., Neves A.M., Vassil Rodrigues-Pousada C.; "Cloning and characterization extension protein-encoding fus Gene 139:201-205(1994).
                                                                                                                                                                                            Nucleic
[15]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Two ubiquitin-long-tail fusion direct repeats in barley."; Gene 94:165-171(1990).
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[9]
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MEDLINE=91057134; PubMed=2173830;
Perrey R., Warskulat U., Wink M.;
"Molecular cloning of a cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christensen A.H., Quail P.H.; "Sequence analysis and transcriptional polyubiquitin transcripts from maize."; Plant Mol. Biol. 12:619-632(1989).
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J. Biol. Chem.
                                                                                                                     SPECIES=L.albus;
MEDLINE=94156199;
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MEDLINE=86274685; PubMed=2426105;
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STRAIN-CV. BOMI;
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sion genes from Lupinus albus."
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SEQUENCE FROM N.A. (UBI3).
SEQUENCE FROM N.A. (UBI3).
SPECIES=L.esculentum; TISSUE=Root;
SEDLINE=92032784; PubMed=1657246;
MEDLINE=92032784; PubMed=1657246;
HOffman N.E., Ko K., Milkowski D., Pic
"Isolation and characterization of tor
"Isolation the ubiquitin gene ubi3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of a ubiquitin-ribosomal protein g
and expression of its promoter in transgenic
plant Mol. Biol. 24:119-127(1994).
                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
NADH-ubiquinone oxidoreductase B12 subunit
(Complex I-B12) (CI-B12).
                                                                                                                                                                                                                                                                                                           Davies K.M., King G.A.;
Davies K.M., King G.A.;
"Isolation and characterization of Asparagus officinalis L.
clones encoding two forms of ubiquitin mRNA.";
clones encoding two forms of 21:153-159(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-N. sylvestris; TISSUE-Leaf; MEDLINE-93099242; PubMed-1281439; Genschik P., Parmentier Y., Durr A
                                                                        Q02365;
01-JUL-1993
                                                                                                                BOVIN
                                                                                                                                                                                                                                                            SPECIES=O.sativa;
MEDLINE=93271454;
Nishi P., Hashimot
                                                                                                                                                                                                                                                                                                                                                                                                                       "Ubiquitin genes are differentia:
cultures of Nicotiana sylvestris
stresses.";
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MEDLINE-93004476; PubMed-1327270;
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 Bos taurus (Bovine).
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MEDLINE=94154225; PubMed=8111011;
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to H., Kidou S.I
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P49634;
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                                                           Biochim. Biophys. Acta 1218:109-111(1994).

-:- FUNCTION: INVOLVED IN THE ATT-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walker J.E., Arizmendi J.M., Dupuis A., Fearnley I.M., Finel Medd S.M., Pilkington S.J., Runswick M.J., Skehel J.M.; "Sequences of 20 subunits of NADH: ubiquinone oxidoreductase bovine heart mitochondria. Application of a novel strategy f sequencing proteins using the polymerase chain reaction."; J. Mol. Biol. 226:1051-1072(1992).
        <del>+</del> +
                                                                                                                                                                                                                                                                               Acanthamoeba castellanii (A
Eukaryota; Acanthamoebidae;
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Unpublished observations (
-!- FUNCTION: TRANSFER OF
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BIOGENESIS.
SUBCELLULAR LOCATION:
MISCELLANEOUS: THIS PI
                                                                                                                                                               Acanthamoeba
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F ELECTRONS FROM NADH TO THE RESPIRATORY
ELECTRON ACCEPTOR FOR THE ENZYME IS BEL
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UBIQ_PHYIN

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plant Mol. Biol. 17:799-811(1991).

Plant Mol. Biol. 17:799-811(1991).

-i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF

CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE

CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE

CELLULAR PROTEINS, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended Bioinformatics and the Extended Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ISOLATE 88069;
STRAILNE-92003691; PubMed-1655113;
Pieterse C.M.J., Risseeuw E.P., Davidse L.C
Pieterse C.M.J., Risseeuw E.P., Davidse L.C
Pieterse C.M.J., Risseeuw E.P., Davidse L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
SEQUENCE
                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              modified and this statement is not removed entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- MISCELLANEOUS: THIS UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH 3 EXACT HEAD TO TAIL REPEATS. THERE IS A FINAL
AMINO-ACID (ASN) AFTER THE LAST REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ubiquitin
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                                                            EMBL; X55717; CAA39250.1;
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HSSP; P02248; 1UBI.
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CONJUGATION TO ACCEPTOR PROTEINS.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thymosin beta-a.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91955;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
Nuclear protein; Polyprotein.
SITE 48 48 NECE
                                                                                                                                                                                                                                                          ProDom; PD005116; Th
                                                                                                                                                                                                                                                                                                Pfam; PF01290; Thymosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Fujiki K., Nakao M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYBA_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  EMBL; AB028456; BAA96492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                              Actin-binding;
                                                                                                                                                                                                                                     PROSITE; PS00500; THYMOSIN_B4; 1.
                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7962
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                                      VPGSQHIDSQKKA
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  LPTKEDIDQEKKA
                                                                                 Similarity6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 38...
8; Conservative
                                                                                                                                                                                                                                                                                                                            IPR001152; Thymosin_b4.
                                                                                                                                                                          45
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                                                                                      Conservative
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6 AA;
                                                                                                                                                                        AΑ;
                                                                                                                                                                                                                 Cytoskeleton.
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                                                                                                                                                                                                                                                                                Thymosin_b4; 1.
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8580 MW;
40
                                                                                                                                                                        5063 MW;
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                                                                                                    31.1%; 46.2%;
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                                                                                                        Score 33; Pred. No.
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Pred. No.
                                                                                                                                                                        BY SIMILARITY.
D05B4129A422EB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS
98F084FE7F3A456F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NECESSARY FOR BRANCHED-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                    Mismatches
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75;
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62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                             <u>ب</u>
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                                                                                                                             Length 45
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                                                                                    Indels
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RESULT 10

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TYBO_TORMA
ID TYBO_T
AC Q91980
DT 01-MAR
DT 01
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Best Local 9
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TYBO_TORMA STANDARD,

Q91980;

Q1980;

Q1-MAR-2002 (Rel. 41, Created)

Q1-MAR-2002 (Rel. 41, Last sequence update)

Q1-MAR-2002 (Rel. 41, Last annotation update)

Thymosin beta-10 (Thymb10).

Torpedo marmorata (Marbled electric ray).

Torpedo marmorata (Marbled electric ray).

Elkaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;

"Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                         UBIQ_ACECL
P42739;
01-NOV-1995
01-NOV-1995
01-NOV-1995
               Frank S., Menzel D.;
Frank S., Menzel D.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN THE ATP-DEFENDENT SELECTIVE DEGRADAT
-i- FUNCTION: THE MAINTENANCE OF CHROMATIN STRUCTURE,
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RI
                                                                                                                                                                                                                                             Acetabularia cliftonii.
Eukaryota; Viridiplantae;
Dasycladaceae; Acetabulari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01290; Thymosin; 1.
ProDom; PD005116; Thymosin_b4; 1.
SMART; SM00152; THY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays an important role in the organization of cytoskeleton. Binds to and sequesters actin monomers (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Electric lobe;
O'Regan S., Matz V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actin-binding; Cytoskeleton. INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation in yeast.";
  ÷
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=3137;
                                                                                                                                                                                                                                                                                                                          Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ276369; CAB76965.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00500; THYMOSIN_B4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Torpedo electric lobe cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LPTKETIDQEKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic (By similarity SIMILARITY: BELONGS TO THE THYMOSIN BETA FAMILY.
BIOGENESIS.
SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytoskeleton. Binds to and sequence therefore inhibits actin polymerization (By similarity). currently LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                            (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                             Acetabularia
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
  LOCATION:
                                                                                                                                                                                                                                                                                                                                            32,
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                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence
Last annotation
Nuclear and
                                                                                                                                                                                                                                                                 Chlorophyta; Ulvophyceae; Dasycladales;
                                                                                                                                                                                                                                                                                                                                            sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
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Pred. No.
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63D5D49977A2E351
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on update)
cytoplasmic
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                                                                                               DEGRADATION OF
                                                AND RIBOSOME
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                                                                                                                                                                                                                                                                                                                                              APT K.E., Grossman A.R.;

APT K.E., Grossman A.R.;

"A polyubiquitin cDNA from a red alga.";

"A polyubiquitin cDNA from a red alga.";

"A polyubiquitin cDNA from a red alga.";

"Plant Physiol. 99:1732-1733(1992).

-1- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENNANCE OF CHROMATIN STRUCTURE, THE CELLULAR PROTEINS, THE MAINTENNANCE OF CHROMATIN STRUCTURE, THE CELLULAR PROTEINS. THE MAINTENNANCE OF CHROMATIN STRUCTURE, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
01-NOV-1995
01-OCT-1996
Ubiquitin.
                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Apt K.E., Grossman "A polyubiquitin c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
VARIANT
VARIANT
                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aglaothamnion.
NCBI_TaxID=2765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aglaothamnion neglectum.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGLNE
                                                                                                                                                                                         between
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P42740;
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Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
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                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restricted the state of the s
                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH SIX HEAD TO TAIL REPEATS. THERE IS ONE ADDIT
AMINO-ACID (MET) AFTER THE LAST REPEAT.
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  M88684;
P02248;
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  AAA72126.1;
1UBI.
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34,
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Last sequence update)
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E -> Q (IN ONE OF THE REPEATS).
R -> L (IN ONE OF THE REPEATS).
34D636389D09903F CRC64;
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                                                                                                                  Usage
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THERE ARE TWO
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Best Local
                Pfeifer K
Batel R.,
                                                                                                                                    SPÉQUENCE FROM N.A. (UBQ-2).
SPÉCIES-C.e.Legans; STRAIN-BRISTOL N2;
SPÉCIES-C.e.Legans; STRAIN-BRISTOL N2;
MEDILINE-96018742; PubMed-7556908;
Jones D., Candido P.M.;
"A portable regulatory element directs
Caenorhabditis elegans ubiquitin gene u
Dev. Biol. 171:60-72(1995).
                                                                                                                                                                                                                                                                                                 Graham R.W., van Doren K., Bektesh S., C
"Maturation of the major ubiquitin gene
elegans involves the acquisition of a tr
J. Biol. Chem. 263:10415-10419(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taich A.,
Submitted
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(UBQ-1 OR UBIA OR F25B5.4)
Caenorhabditis elegans, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UBIQ_CA
P14792;
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graham R.W., Jones D., Candidio E.P.M.;
"UbiA, the major polymbiquitin locus in Caenorhabditis elegans, unusual structural features and is constitutively expressed."; mol. Cell. Biol. 9:268-277(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=C.elegans;
MEDLINE=89181579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239, 6047;
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01-APR-1990 (Rel.
01-FEB-1996 (Rel.
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VARIANT
                                                      SPECIES-G.cydonium;
MEDLINE-94110294; P
                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=C.elegans;
MEDLINE=88273146; PubMed=2839490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-C.elegans; STRAIN-BRISTOL
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Pfam; PF00240; ubiquitin; 1.
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r K., L.
R., Mueller
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33,
                                                      PubMed=8282761;
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38.1%;
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Pred.
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CONJUGATION TO ACCEPTOR PROTEINS.
L -> I (IN ONE OF THE REPEATS).
I -> N (IN ONE OF THE REPEATS).
I -> L (IN ONE OF THE REPEATS).
DE993623CCFE9B52 CRC64;
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ne transcript in Caenorhabditis
trans-spliced leader.";
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                                                                                                                                                         of the gonad."
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RESULT 14
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AC P1-APR
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RP SEQUEN
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Best Local (
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01-APR-1990
01-NOV-1997
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SEQUENCE
Callis J., Pollmann L., Shanklin J., Wettern M., V "Sequence of a cDNA from Chlamydomonas reinhardii ubiquitin 52 amino acid extension protein."; Nucleic Acids Res. 17:8377-8377(1989).
                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
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-i- FUNCTION: INVOLVED IN THE AATP-DEPENDENT SELECTIVE DEGRADATION CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UBIQ_CHLRE
P14624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; F25B5.4; CE01921.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     UBI1 AND UBI3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
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                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Obiquitin.
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BL; U23172; AAC46525.1; ALT_TERM.
BL; M21321; AAA28153.1; -
BL; L31492; AAC37252.1; ALT_TERM.
BL; X70917; CAA50268.1; ALT_TERM.
BL; X70917; GA50268.1; ALT_TERM.
R; A30126; A30126.
R; A28804; A28804.
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MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH 11 EXACT HEAD TO TAIL REPEATS. THERE ARE TWO
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CONJUGATION TO ACCEPTOR PROTEINS
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=90136711; PubMed=2559328;
Wong S., Campbell D.A.;
"A polyubiquitin gene from Trypanosoma brucei.";
"A polyubiquitin gene from Trypanosoma brucei.";

Nucleic Acids

Res.

18:7181-7181(1990)

Trypanosoma

Wong S., Morales T.H., Campbell D.A.; "Ubiquitin-EP52 fusion protein homologs from

MEDLINE=91088342; PubMed=2175891;

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P15174; 01-APR-1990 01-APR-1990 01-FEB-1995

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STANDARD;

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Eukaryota; Euglenozoa; NCBI_TaxID=5702;

Kinetoplastida; Trypanosomatidae; Trypanosoma

Trypanosoma brucei brucei

Ubiquitin.

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Matches 8
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EMBL; X60826; CAA43216.1;
PIR; S06598; UQKM
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PROSITE; PS00299; UBIQUITIN_1;
PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
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"Ubiquitin in a lower plant. Characterization
DNA and RNA from Chlamydomonas reinhardii.";
Eur. J. Biochem. 202:197-204(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (UBI3). MEDLINE=92037644; PubMed=1657605;
                                                                                                                                             Nuclear protein; Polyprotein.
SITE 48 48
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PRINTS; PR00348; UBIQUITIN.
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1 GATFQVEVPGSQHIDSQKKAI
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SUBCELLULAR LOCATION: Nuclear and cytoplasmic SUBCELLALAR LOCATION: Nuclear and cytoplasmic MISCELLANDOS: UBI1 IS SYNTHESIZED AS A POLYPI OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                            Similarity
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6 AA;
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                                                                                                  MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS
C42936277D1E9B52 CRC64;
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Pred. No. 1.6e+02;
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                                            Mismatches
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EMBL; X54641; CAA38453.1; -.
EMBL; X56462; CAA38454.1; -.
EMBL; X56511; CAA39863.1; -.
EMBL; X56511; CAA39864.1; -.
PIR; S07998; UQUT.
PIR; S14197; S14197.
PIR; S14197; S14197.
HSSP; P02248; 1UBI.
InterPro; IPRO00626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
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"Genomic and transcriptional linkage of the genes for calmodulin, Ef-
hand 5 protein, and ubiquitin extension protein 52 in Trypanosoma
brucei.";
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MEDLINE=93109304; PubMed=8380221;
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SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN

PRECURSOR WITH 5 OR 6 EXACT HEAD TO TAIL REPEATS. SOME UBIQUIT

GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way in the state of the
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FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
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CONJUGATION TO ACCEPTOR PROTEINS.
C53759576F0C8E47 CRC64;
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ches 10;
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GenCore version Copyright (c) 1993 - 2002

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Maximum Match
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Q9JRI4
Q97QB1
Q97PZ4
Q9M4A4
Q9M4H3
Q9M4H3
Q9QYJ8
                        036044
Q07188
036058
036043
Q9GMA0
Q9RJ40
Q96HT2
                                                                                                                                     ij
                                                       Q42153
                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                         residues
                              O9syf4 arabidopsis
O9jri4 neisseria m
O9jqhi streptococc
O9ypz4 streptococc
O9m4a4 cucumis mel
O9m4h3 vitis vinif
O9gyj8 rattus norv
O19274 saguinus oe
O42153 arabidopsis
O36044 mastigamoeb
O7188 saccharomyc
O35058 mastigamoeb
09gma0
09rj40
096ht2
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                                                                                                                                    Description
      streptomyce
                       mastigamoeb
               sus scrofa
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ALIGNMENTS

RESULT 1 Q9SYF4

Q9SYF4, Q9SYF4; Q1-MAY-2000 (TIEMBLTel. 13, 01-MAY-2000 (TIEMBLTel. 13, 01-DEC-2001 (TIEMBLTel. 19,

Created)
Last sequence update)
Last annotation update)

core eudicots; Rosidae;

PRT;

91

F15I1.6 PROTEIN. F15I1.6.

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Best Local S
Matches 10
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InterPro: IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 2.
SEQUENCE 91 AA; 10142 MW; E8766823D6450267 CRC64;
                                                                                                                                                                                                                                                                      STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu Li J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Altafi
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
58 GKTFNLEVKGSEIIQQVKNMI 78
                           1 GATFQVEVPGSQHIDSQKKAI 21
                                                          l Similarity
10; Conserv
                                                          Conservative
                                                                        41.5%;
                                                                          Score 44; DB 10;
Pred. No. 6.9;
                                                          Mismatches
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IS66 FAMILY
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Q9JRI4;
01-OCT-2000
01-OCT-2000
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Science 287:1809-1815(2000).
EMBL; AL162755; CAB84626.1;
EMBL; AE002469; AAF41600.1;
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                             SEQUENCE FROM N.A.
STRAIN-TIGR4;
                                                                                                                                                                                                                                            Streptococcus pneumoniae
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Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sub
NCBI_TaxID=65699, 491;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN NMA1380.
NMA1380 OR NMB1218
MEDLINE-21357209;
                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                           Bacteria; Firmicutes;
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STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
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                                                                                                                                      NCBI_TaxID=1313;
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8; Conser
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   PubMed=11463916;
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10228 MW; (
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38.1%;
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A Tettelin H., Nelson K.E., Faults.

A Tettelin H., Nelson K.E., Faults.

A Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Doosum N.C., Peterson J.D., RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., RA Duryam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., RA McDonald L.A., Feldbyum T.V., Angiuoli S., Dickinson T., Hickey E.K. RA McDonald L.A., Feldbyum T.V., Angiuoli S., Dickinson T., Hickey E.K. RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., RT "Complete genome sequence of a virulent isolate of Streptococcus RT pneumoniae.";

RT "Complete genome sequence of a virulent isolate of Streptococcus RT pneumoniae.";

RL Science 293:498-506(2001).

DR EMBL; AE007441; AAK75537.1; -.
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01-OCT-2001
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Science 293:498-506(2001).
Science 293:498-506(2001).
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                                                                                                                                                                              SEQUENCE 79 AA;
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VEIPOSRRFDSKKR
                                          VEVPGSQHIDSQKK
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SP1314; -.
                                                                                       Similarity 7; Conserv
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Y ELEMENT, ORF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7209; PubMed=11463916;
Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
                                                                                                                                                                              9294 MW;
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Pred. No.
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Matches 6
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Best Local
    Q9QYJ8;
Q9QYJ8;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                       Davies C., Robinson S.P.;
"Differential screening indicates a dramatic change in mRNA properties of the properties of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. SHIRAZ; TISSUE-FRUIT;
MEDLINE-20177861; PumMed-10712544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vitis vinifera (Grape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation updat
PUTATIVE METALLOTHIONEIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9M4H3
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EMBL; AJ251872; CAB88871.1; -.
InterPro; IPR002182; NB-ARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcia-Mas J., van Leeuwen H., Monfort A., Puigdomenech P., Arus P.; "Cloning and mapping of resistance gene ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumis melo (Muskmelon).

Cucumis melo (Muskmelon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cúcurbitales; Cucurbitaceae; Cucumis.
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PUTATIVE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9м4Н3;
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=29760;
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                                                                                                                                                                                           ATVVMEVPAAQHEGSCK 51
                                                                                                                                                                                                                         ATFQVEVPGSQHIDSQK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00931; NB-ARC; 1.
                                                                                                                                                                                                                                                                                                Similarity
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    (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                            65 AA;
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Created)
Last sequence update)
Last annotation update)
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Pred.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                          B5EA7D8D7B9170D4 CRC64;
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34;
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33;
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Best Local :
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                      ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC II; Transmembrane.
NON_TER 1 1
NON_TER 83 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 3-30 FROM N.A.
STRAIN-B95-8; TISSUE=BLOOD;
MEDLINE=97252963; PubMed=9098421;
BidWell JL., Lu P., Wang Y., Zhou K., Clay
"DRB, DQA, DQB and DPB nucleotide sequences
                                                                                                                                                                                                                                                                      Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF027966; AAB84042.1; -. InterPro; IPR000353; MHC_II_beta. Pfam; PF00969; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=B95-8; TISSUE=BLOOD; de Groot N.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saguinus oedipus (Cotton-top tamarin)
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           019274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alternative exon usage in the 3'region glycosylphophatidylinositol-anchored and decay-accelerating factor";
Immunogenetics 51:129-137(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WISTARST;
MEDLINE-20130146; PubMed=10663575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Immunogenet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ven
Mammalia; Eutheria; Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
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40
                                        2 ATFQVEVPGSQHIDSQK 18
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AVTELGLPAAEHLNSQK
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                                                                                Similarity 6; Conserv
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                                                                                                                                                                    83 AA;
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                                                                                   Conservative
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                                                                                                                                                                      9737 MW;
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Rodentia;
                                                                                                       36.8%;
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56
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                                                                                   7;
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                                                                                                         Pred.
                                                                                                                           Score 39;
                                                                                                                                                                      465CF7063360C9BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clay T.M., Bontrop R.E.; ences of Saguinus oedipus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a
                                                                                                                             DB
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ni; Callitrichidae; Saguinus.
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                                                                                                                           Length 83;
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Q42153;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-DR-1999 (TrEMBLrel. 09, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RELATIVE TO UBIQUITIN, PARATHYROID.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Q07188;
Q07188;
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TESPO 2248; JUBI.
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                                                                                                                                                                                                                            InterPro; IPR000626; Obiquitin. Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                               Mastigamoeba balamuthi.
Eukaryota; Pelobiontida;
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HSSP; P02248; 1UBI.
InterPro; IPR000256; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
SEQUENCE 44 AA; 4860 MW; DB
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Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; Z26872; CAA81485.1; -.
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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TISSUE=CELL SUSPENSION CULTURE OF
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polyubiquitin genes in Phreatamoeba
rna: Phylogenetic implications.";
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Pred. No. 48;
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Pred.
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EMEL; AJ000656; CAA04204.1; -
EMBL; AJ000660; CAA04208.1; -
EMBL; AJ000655; CAA04203.1; -
EMBL; AJ000659; CAA04207.1; -
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01-NOV-1996
01-JUN-2001
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InterPro; IPR000626; Ubiquitin.
Pfam, PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SMART; SM00213; UBQ; 1.
PROSITE; PS50053; UBIQUITIN_2;
SEQUENCE 47 AA; 5220 MW; BI
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MEDILINE=88061630; PubMed=6095120;

Oezkaynak E., Finley D., Varshavsky A.;

Nature 312:663-666(1984).

EMBL; X01473; CAA2575.1; -.

EMBL; X01473; CAA2575.1; -.

SGD; S0003962; UBI4.

InterPro; IPR000626; Ubiquitin.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                    Mastigamoeba balamuthi.
Eukaryota; Pelobiontida;
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UBI4 AND YLL039C
                                                                                    SEQUENCE
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Mastigamoeba balamuthi.

UBIQUITIN (FRAGMENT)

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RESULT

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O1-MAR-2001 (TrEMBLrel. 1
O1-MAR-2001 (TrEMBLrel. 1
O1-JUN-2001 (TrEMBLrel. 1
CD5 ANTIGEN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98251471; PubMed-9589566;
Appleyard G.D., Wilkie B.N.;
Porroine CD5 gene and gene product identified on the species conserved cytoplasmic domain sequences.";
Species conserved cytoplasmic domain sequences.";
Tamminol. Immunopathol. 60:275-283(1998).
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PROSITE;
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                            Appleyard G.D., Wilkie B.N.; Submitted (AUG-2000) to the EMBL; AF291867; AAG02103.1; NON_TER 1 1 1 73 73
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Redenbach M., Kieser H.M., Denapaite D., Eichner A
Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).

EMBL; AL132644; CAB59444.1; -.

Hypothetical protein.

SEQUENCE 77 AA; 8352 MW; 86EA16403CC7B7A1 CRC6
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Labile toxin (LT-B	Recombinant exotox	Recombinant exotox	Recombinant exotox	Recombinant exotox	LTB	E. coli LTB protei	LTB	LTB	i LTB	E coli verotoxin-1		E. coli heat-labil	Escherichia coli v	ADP-ribosylating t		Sequence of sub-un	V-1 an	coli heat-		usio	e of LT		LTB prote	LTB	ш			ra strai	Cholera toxin B su	Plant-optimized E.	id seque	Cholera toxin B su	B subunit of the h

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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-l}$ -

2000-256943/22.

Disclosure; Page 15;

62pp; English

coli heat

labile

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RESULT 2
AAW04857
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- -- Tocal Similarity
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                  gene
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                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholera toxin B subunit; enzyme; antigen; immunogen; allergen;
enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin;
                                                              Bordetella –
                                                                                   Recombinant
                                                                                                                                                                                                   Klein
                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04857 standard; Protein; 103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to peptide fragments of the Escherichia coli h
ile enterotoxin (Etx) and its closely related homologue, cholera
in (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                       of,
                                       cholera B toxin,
                                                                                                                               1996-425088/42.
DB; AAT38038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                   ,HM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                     constructs for expressing and opt. secreting proteins in comprise Bordetella promoter coupled to non-Bordetella, a B toxin, gene or coupled to non-Bordetella leader and
                                                                                                                                                                                                   Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                           95US-0393334
                                                                                                                                                                                                                                                                                                                                       96WO-CA00107.
                                                                                                                                                                                                   , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor;
                                                                                                                                                                                                 Yacoob RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106; DB 21;
Pred. No. 5.1e-11;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heterologous gene; leader; promoter
                                                                                                                                                                                                 Zealey GR
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RESULT 3
AAR94939
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, fha promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit S1 leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a novel synthetic cholera toxin B gene (ctb) and the hmw1 and hmw2 genes of Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-Bordetella leader sequence for secretion of a gene product which may or may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, lymphokines, immunoglobulins or their
                                                                                                                                  Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                      Disclosure;
                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                 WPI; 1996-230602/23.
                                                                                                                                                                                                                              Arntzen
                                                                                                                                                                                                                                                                                                       24-0CT-1994;
                                                                                                                                                                                                                                                                                                                                   24-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                 02-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        adjuvant; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile enterotoxin B subunit (LT-B) E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR94939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR94939 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 100.0%;
1 Similarity 100.0%;
21; Conservative
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                                                                                                                                                                                                                                                          TULANE EDUCATIONAL FUND
                                                                                                                                                                                 AAT18799, AAT18800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 AA;
                                                                                                     Page 100-101; 130pp; English.
                                                                                                                                                                                                                             Clements
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Pred. No. 3.2e-10;
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                                                                                                                                                                                                                              SH
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A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an orral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals

using transgenic plants, where the plants express bacterial antigens

adjuvants.

provides

immunogens and

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AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; heat labile enterotoxin B subunit; LTB; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06606 standard; Protein; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                              Claim 3;
                                                                                                                                                                                    Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                  WPI; 1996-506108/50.
N-PSDB; AAT43576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                      Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                           Page -; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen; broad spectrum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 AA;
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Enterotoxigenic
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95
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"wild-type His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "wild-type Ala
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Pred. No.
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No. 3.2e-10;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a
AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid
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                                                                                                                                                                      Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                           Claim 4;
                                                                                                                                                                                                                                                                                                                                                  Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vomiting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW06605)
                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                (LEBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                          (HOLM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                          1996-506108/50.
DB; AAT43577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                   LEBENS M
                                                                                                                                                                                                                                                                                                                                                                                                                       HOLMGREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .
                                                                                                                           Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae
Enterotoxigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                     Lebens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95SE-0001682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-SE00570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                           32pp;
                                                                                                                                                                                                                                                                                                                                                                                                   ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= substitution
/note= "the first 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wild-type cholera toxin B subunit replaced with the first 25 amino a of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e 106; DB 17;
. No. 3.2e-10;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acids of mature
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diarrhoea
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RESULT 6
AAW808088
ID AAW8
XX AAW8
AXC AAM8
XX Chol
DT 29-j
CX AMI
XX Chol
KW Anti
XX Chol
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FA (KI)
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Matches
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                                                          This is the amino acid sequence or the country control as the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines
                                                                                                                                                                                                                                                                                                                                                                                       New mutant cholera toxin selected from subunits/derivatives - effective as an with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin induced illness, e.g. diarrhoea
     Sequence
                                                       administered subcutaneously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KIYO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and vomiting, in humans and animals.

Note - This sequence does not appear in the specification,
a claimed mutant sequence of mature cholera toxin B subuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substitutions impart LTB-specific epitope characteristics immunogenic mature CTB. The hybrid molecules have increase
                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1B; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kiyono H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9845324-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW80808 standard; protein; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW80808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-594478/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) KIYONO H.
) MCGHEE J R.
) TAKEDA Y.
) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Similarity
21; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAMAMOTO S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcghee JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US06725
                                                                                                                                                                                                                                                                                     acid sequence of the cholera toxin B subunit used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mucosal; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nontoxic subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106; DB 17;
Pred. No. 3.2e-10;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                               a group comprising nontoxic adjuvant when coadministered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adjuvant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        have increased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
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65 21 Query Match Best Local S Matches 21

Similarity 21; Conserv

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Best Local
                                                                                  The invention relates to a recombinant AB5B subunit protein comprising at least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (CTB) can be used in the treatment of autolimmune diseases e.g. rheumatoid arthritis, encephalomyelitis (or other neuron
                          demyelinating diseases) and diabetes. The rCTB or other B subunits invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a CTB variant protein, NCBI GenBank No. GI 1421511.
                                                                                                                                                                                                                                                                                 Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
Sequence
                                                                                                                                                                                                                                                                    treating
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-281974/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogen; autoimmune disease; neuron demyelinating disease; rCTB; infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62367;
                                                                                                                                                                                                                                        Disclosure; Page 67-68; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Handley
                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200127144-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V. cholera cholera toxin B (CTB) protein variant (GI 1421511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001
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                                                                                                                                                                                                                                                                      autoimmune diseases
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103
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                                                                                                                                                                                                                                                                                                                                                                           Haaparanta T,
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                                                                                                                                                                                                                                                                                                                                                                             Ewalt KL;
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Pred. No. 3.2e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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RESULT

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RESULT 9
AAB62369
ID AAB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant AB5B subunit protein comprising a mutation that alters number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogen; autoimmune disease; neuron demyelinating disease; rCTB;
infection; parasitic; immunosuppressive; antiarthritic; antirheumatic;
antidiabetic; neuroprotective; vaccine; variant.
                      V. cholera cholera toxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V. cholera cholera toxin B
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                                                                        29-JUN-2001
                                                                                                                        AAB62369
                                                                                                                                                                       AAB62369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Handley
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                                                                                                                                                                                                                                                                                          GATFQVEVPGSQHIDSQKKAI
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21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haaparanta T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation;
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                      (CTB) protein variant
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    e 106; DB 22;
. No. 3.2e-10;
smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholera
                         (GI 2781121).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GI 1421525)
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
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RESULT 10
AAR04163
ID AAR04
XX AR04
XX AR04
XX IO-SE
XX Chole
XX Chole
XX Chole
XX Chole
XX Chole
XX Chole
XX IO-SE
XX I
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misc_difference

Location/Qualifiers 18..18

/*label= His or

Tyr

/*label= signal peptide /*note= absent from mat

mature

protein

region

cholera toxin Cholera 10-SEP-1990

B-subunit; hybrid protein; heterologous IgA active antigen

Toxin

B-subunit.

(first entry)

AAR04163;

AAR04163 standard;

protein;

118

B

synthetic

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Qy
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                                                                    Matches
                                                                                      Query Match
Best Local
                                                                                                                                                                     least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (TCB) can be used in the treatment of autoimmune diseases e.g. rheumatoid arthritis, encephalomyelitis (or other neuron demyelinating diseases) and diabetes. The rCTB or other B subunits of the invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a CTB variant protein, NCBI GenBank No. GI 2781121 (Ogawa 41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; infection; parasitic; immunosuppressive; antiarthritic; antirheuma antidiabetic; neuroprotective; vaccine; variant.
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant AB5B subunit protein comprising least one mutation, where the mutation alters the number of amino acid
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                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Handley HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000;
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46
                 1 GATFQVEVPGSQHIDSQKKAI
 GATFOVEVPGSQHIDSQKKAI
                                                                                      Similarity
                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                Page 68-69; 78pp; English.
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haaparanta T,
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                                                                                      100.0%;
 66
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                                                                    0
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                                                                  Score 106; DB 22;
Pred. No. 3.3e-10;
Mismatches 0;
                                                                                                  Length
                                                                    Indels
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Best Local :
                                                                                                                                                                                                                               immunogen; autoimmune
infection; parasitic;
antidiabetic; neuropro
        Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature cholera toxin B-subunit is obtained cleaved off. There is an Ochre codon at pos downstream from it is part of a plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hybrid protein, useful in vaccines - contains cholera toxin b subunit and heterologous IgA active
                                                                                  Handley
                                                                                                      (ACTI-) ACTIVE BIOTECH AB.
                                                                                                                           08-OCT-1999;
                                                                                                                                              05-OCT-2000; 2000WO-US27607
                                                                                                                                                                    19-APR-2001.
                                                                                                                                                                                         WO200127144-A2
                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                             AB5B subunit protein;
                                                                                                                                                                                                                                                                                                        29-JUN-2001
                                                                                                                                                                                                                                                                                                                            AAB62374;
                                                                                                                                                                                                                                                                                                                                                AAB62374 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                             1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                  coli LTB protein variant (GI: 1395122).
                                                              2001-281974/29
                                                                                                                                                                                                                                                                                                                                                                                                   GATFQVEVPGSQHIDSQKKAI 76
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DB; Q04046.
                                                                                  HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative
                                                                                 Haaparanta
                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                neuroprotective;
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                                                                                                                           99US-0158561
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                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                              mutation; recombinant; cholera toxin B; CTB; disease; neuron demyelinating disease; rCTB; LTB immunosuppressive; antiarthritic; antirheumatic; otective; vaccine; heat labile toxin B; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martial
                                                                                 Τ,
                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                  Ewalt KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 11;
Pred. No. 3.8e-10;
; Mismatches 0;
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RESULT 12
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Best Local S
Matches 21
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                                            Fig
                                                                    encoding
                                                                                Live recombinant vaccine for malaria comprising attenuated entero-invasive
                                                                                                                    N-PSDB;
                                                                                                                                                       Brey RN,
                                                                                                                                                                                                                                                                                                                                                      кеу
                                                                                                                                                                                                                                                                                                                                                                                                                            B subunit; heat-labile enterotoxin; LT-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    B subunit of the heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP93561;
                                                                                                                                WPI; 1989-114399/15
                                                                                                                                                                                                         02-OCT-1987;
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                                                                                                                                                                                                                                                                               W08902924-A
                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                  circumsporozoite protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 70;
                                                                                                                                                                                 (PRAX-)
                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 GATFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATFQVEVPGSQHIDSQKKAI 21
                                            p. 3/17; 105pp; English
                                                                                                                      AAN90747
                                                                                                                                                                                 PRAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                   epitope of malaria parasite
                                                                                                                                                       Majarian WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                     epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                 BIOLOGICS
                                                                                                                                                                                                        87US-0104735
                                                                                                                                                                                                                                88WO-US03376
                                                                                                                                                                                                                                                                                                                    23..124
                                                                                                                                                                                                                                                                                                     /note≃"Mature LT-B"
                                                                                                                                                                                                                                                                                                                             /note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78pp; English.
                                                                                                                                                        Pillai S,
                                                                                                                                                                                 IZ
                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106; DB 2
Pred. No. 4e-10;
Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                         Hockmeyer WT
                                                                                  bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LT-B) derived
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; malari live recombinant vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                 contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                              malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. col1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region or a repeat region of circumsporozoite protein antigen (CS) (AAP93560

QY

Вb

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RESULT 13
AAW06605
ID AAW06
XX AAW06
XX AAW06
XX AAW06
XX AAW06
DT 06-AI
XX Heat
KW Heat
KW Immu
KW vomi
XX Yib
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local !
                                                                              AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06606 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be
                                                                                                                                                                                                                                                                                                                                                                                          Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT43575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cholera toxin B subunit, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOLM/) HOLMGREN J.
(LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vomiting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; heat labile enterotoxin B subunit; LTB; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW06605 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multivalent.
                         hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen; antigen; broad spectrum; cross reactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1996-506108/50.
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Immunogenic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                              Fig 1; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lebens MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95SE-0001682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-SE00570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= sig_peptide
22..124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for hybrid immunogenic toxin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps.
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66

GATFQVEVPGSQHIDSQKKAI

86

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GATFQVEVPGSQHIDSQKKAI 21

Matches

21;

Conservative

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Gaps

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RESULT 14
AAM59770
ID AAM59
XX AAM59
XX AAM59
XX DAM59
XX DAM59
XX DAM60
DT 12-OC
XX Beta-
KW immun
KW FSH;
XX Esche
XX WO982
XX W0982
XX HIMMUN
KW PSH;
XX HIMMUN
KW PSH;
XX HIMMUN
CC Indrum
CC in
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                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                     This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, partic for increasing animal fertility by inducing antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bagdasarian M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-subunit of heat labile enterotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSH; sperm; ova;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW59770
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                                                                                                                                                     in edible plants or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lmmunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI
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DB; AAV41573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATFQVEVPGSQHIDSQKKAI
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                      124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Score 106; DB 1
Pred. No. 4e-10;
; Mismatches
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RESULT 15
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                                                                                                                                                                                                                                                                                                                   This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized CDNA. The CDNA sequence contains plant-preferred codons and eliminates sequence motifs associated with plant-codon graph of the second codon is changed from ANT encoding the spurious mRNA processing. The second codon is changed from ANT encoding CD Asn to GTG encoding Val, in order to create a NCOI restriction site at the 5' end. Novel polynucleotides encode a mutant LT-A polypeptide or a CC mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CC CT-A polypeptide and where at least one of the codons is altered to a CC plant preferred codon. The polynucleotide further comprises a nucleic cald sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The CC polynucleotides are useful for the transformation of plant cells for the prolynucleotides in transgenic plants to produce edible vaccines, especially coral vaccines in transgenic plants for the prophylactic or therapeutic coral content against E. coli or V. cholerae. The mutant polypeptides are
                                                                                                                       Matches
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals {\bf r}
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 5A-B; 103pp; English.
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N-PSDB; AAA51156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96652 standard; Protein; 124 AA
                                                                                                                                                                                                                                                                                                      also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOYC-) BOYCE THOMPSON INST PLANT RES.
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1998;
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                                                                                                                                                Similarity
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Pred. No. 4e-10;
                                                                                                                                                                            Length 124;
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Search completed: October 24, 2002, 15:20:28 Job time: 34.7377 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
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US-08-467-976-26
US-08-487-976-26
US-08-487-976-26
US-08-487-976-26
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US-08-435-6035-12
S223610-3
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Compugen Ltd.
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US-08-952-337-5
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Sequence 4, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 234, App	Patent No. 5194375	Sequence 36, Appl	Sequence 35, Appl	Sequence 34, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 133, App	Sequence 133, App	Sequence 2, Appli	Sequence 30, Appl

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Holmgren, Jan

APPLICANT: Lebens, Michael R.

APPLICANT: Lebens, Michael R.

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

FILE REFERENCE: 3846/00758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1998-01-05

EARLIER APPLICATION NUMBER: PCT/SE96/00570

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER APPLICATION NUMBER: SE 9501682-0
                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-952-337-6
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LENGTH: 102
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APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-02
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: SE EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 GATFQVEVPGSQHIDSQKKAI 64
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Pred. No. 2.5e-11;
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Tocal Similarity
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Best Local Similarity
                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 103 amino acid
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                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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                                                                                                                                                                                                          TELEFAX: 410-33 TELEX: 065-24567 Simbas
45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                 NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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CITY: Toronto
STATE: Ontario
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MEDIUM TYPE: Floppy disk
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               1 GATFQVEVPGSQHIDSQKKAI 21
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M5G 1R7
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Zealey, Gavin R.
Klein, Michel H.
                                                          Conservative
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                                                                    Score 106; DB 2; Pred. No. 2.5e-11;
                                                          Mismatches
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                                                                                    Length 103;
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RESULT 5
US-09-013-047-2
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Sequence 2, Appr---
Sequence 2, Appr---
No. 5942418
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Best Local Similarity
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/894,526
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COTTONION: PC-DOS/MS-DOS
                                                                                                                                                                                     TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                              APPLICANT: LOOSMOTE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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APPLICANT: Zealey, Gavin R
APPLICANT: Klein, Michel H
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                                                                                      STREET: 330 Un CITY: Toronto STATE: Ontario
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FILING DATE: 01-DEC-1997
                                                                      COUNTRY:
                                                                                                                    ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6th Fl
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                                                     rRY: Canada
M5G 1R7
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M5G 1R7
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                                                                                        Ontario
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) 595-1163
- NO: 2:
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                                                                                                                                                                                                                                                                                 Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 University Avenue
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Pred. No. 2.5e-11;
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                                                                                                                          6th Floor
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OPERATING SYSTEM:

PC-DOS/MS-DOS

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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
rocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: FEBRUARY
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Klein, M
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 103 amino acid
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REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION NUMBER: US 08/472,171
                              ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 416-595-1163
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CITY: Toronto
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                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 GATFQVEVPGSQHIDSQKKAI 65
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REFERENCE/DOCKET NUMBER:
              NAME: Stewart, Michael I REGISTRATION NUMBER: 24973
                                                               CLASSIFICATION:
                                                                                                                                  CLASSIFICATION:
                                                                                                                                                    FILING DATE:
                                                                                                                                                                    APPLICATION NUMBER:
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    Application US/09374597
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065-24567 Simbas
770 TD NO: 2:
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Zealey, Gavin R.
Klein, Michel H.
                                                                                                                                                                                                                                                                                                       Canada
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RY 23, 1995
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1038-964
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Pred. No. 2.5e-11;
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45 GATFQVEVPGSQHIDSQKKAI 65

1 GATFQVEVPGSQHIDSQKKAI 21

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RESULT 7
US-09-191-852-21
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                                                            US-09-191-852-21
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09191852 Patent No. 6194560
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                                                                                                                                                                   REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION: TELEPHONE: 713-651-5151
                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/1:
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: FOX, DAVId L.
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDITION TO STREET: L. STREET: Houston
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                                                                           TYPE: am TOPOLOGY:
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                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 065-24567 Simbas
                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                       103 amino acids
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1301 McKinney, Suite 5100
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                                                                                                                                                      713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq VENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
 Conservative
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            100.0%; Score 106; DB 4; 100.0%; Pred. No. 2.5e-11;
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0;
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No. 2.5e-11;
 Mismatches
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                              Length 103;
 Indels
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Gaps
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US-08-952-337-1

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US-08-952-337-1
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PCT-US95-13376-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-13376-21
                                                                                                     APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                           SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08952337 Patent No. 6019973
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Best Local
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                            NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
ORGANISM: Vibrio cholerae
                                    ENGTH: 123
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: 713-850-0909
TELEPAX: 713-850-0165
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FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: COllege Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
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ZIP: 77027-9095
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1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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RESULT 11
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TYPE: PRT
; ORGANISM: Eschcerichia coli
US-08-952-337-2
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US-08-952-337-2
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; SEQ ID NO 2
TWETH: 123
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Best Local S
Matches 21
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Patent No. 5993820
GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 3846/0D758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edeil, Welter & Schmidt
STREET: 3100 No. 5993820west Center, 90 South Seventh St
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BAGDASARIAN, Michael APPLICANT: IRELAND, James
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 12-NOV-1996
                                                                                                                                                                                                                                                                                            STREET: 3100 No. : CITY: Minneapolis
                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GATFQVEVPGSQHIDSQKKAI 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GATFQVEVPGSQHIDSQKKAI 85
                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
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o. 6019973
                                                                                                                                                                                                                                               55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 100.0%; Score 106; DB 3;
Similarity 100.0%; Pred. No. 3.1e-11;
21; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                               CHIMERIC LTB VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 123;
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; ORIGINAL SOURCE:
US-08-747-410-2
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US-08-292-968-26
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26,
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                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 24-AUG-1S
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                           APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                            REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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STRANDEDNESS: SILLY
STRANDEDNESS: SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 GATFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kettelberger, Denise REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEIN, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sim & McBurney
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(416) 595-1155
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                                                                                                                                                                                                                                                                                                                                   US 08/110,947
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Pred. No. 3.2e-11;
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US-08-467-974-26
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US-08-467-974-26
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                                                                TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                              APPLICATION NUMBER: US 01 FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/110,947
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
                                                                                                                                                                                                                                                                      FILING DATE: 22-AUG-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                         STRANDEDNESS:
                                          TYPE:
                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUI APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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             TOPOLOGY:
                                                    LENGTH:
                                                                                                                                                                      NAME:
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                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION:
                                                                                                                                                                   STEWART, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ontario
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Suite 701, 330 Un
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STEIN, Pene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARMSTRONG, Glen D.
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95.2%;
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Pred. No. 1.7e-10;
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APPLICATION DATA:
US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION UNMBER: US 08/251,121
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                       FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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35
                                                                                                                                  STRANDEDNESS: Sin
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                                                                           Local Similarity
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GETFQVEVPGSQHIDSQKKAI 55
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20; Conservative
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Suite 701, 330 Un
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                                                            Conservative
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95.2%;
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Pred. No. 1.7e-10;
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                                                            Mismatches
                                                                                       Length 93;
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UNO:

OCTERSTICS:

93 amino acids

sirpE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-467-976-26

Query More
Search completed: October 24, 2002, Job time: 13.3934 secs
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                              TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: READ,
APPLICANT: STEIN,
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APPLICANT:
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APPLICATION NUMBER: 1
FILING DATE: 22-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0.)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                              35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                               Local
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ZIP: M5G 1R7
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STATE: Ontario
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lite 701, 330 University Avenue
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ກາດ: 26:
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                                                                                                                               Score 101; DB 3; Length 93; Pred. No. 1.7e-10; O; Mismatches 1; Indels
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
/cgn2_6/ptodata/1/paa/US080_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
/cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
/cgn2_6/ptodata/1/paa/US084_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
/cgn2_6/ptodata/1/paa/US086_COMB.pep:*
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11 US-09-786-648-4

US-08-393-334-2

11 US-08-782-832-15

22 US-08-817-906-21

23 US-09-836-433-20

24 US-09-836-433-20

25 US-09-836-433-22
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(without alignments)
52.114 Million cell updates/sec
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                                                                                                                                                                                        Description
Sequence 15, Appl
Sequence 21, Appl
Sequence 14, Appl
Sequence 20, Appl
Sequence 22, Appl
                                                                                                                    Sequence 2,
                                                                                                                 Sequence 4, Appli
sequence 2, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	S	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ
46	46	46	46	47	47	47	47	48	51	51	51	62	76	76	94	94	94	94	94	94	94	100	100	101	101	101	101	101	101	101	106	106	106	106	106	106	106
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529	365	101	99	484	433	395	369	484	508	448	286	12	15	15	1338	750	461	461	382	382	124	124	124	371	371	371	93	93	93	21	364	351	313	138	138	124	124
18	20	15	21	21	21	26	21	16	19	21	21	21	11	11	18	18	18	14	Ľ	Ľ	21	18	⊢	12	11	U	6	σı	ഗ	21	21	21	21	13	13	18	щ
-09-417-507-	-09-692-058-1	-09-134-000-37	-09-758-463-76	-09-708-427-58	-09-708-427-58	-60-324-109-1951	-708-427-58	A-7	-09-563-99	-09-76	-09-758-44		-08-732-371A	-08-732-371-	-09-402-	-09-402-100-	-09-423-493-	-09-051-315-	US01-08582-	-US01-08582-	-09-760-234-	09-470-124-	us99-30747-	08-829-026-	-08-784-218-	-08-150-305A-	-08-251-121-2	-08-110-947A-	8-110-947-	-09-786-648-	-09-756-983-	-09-756-983-1	-09-756-983-	-914-479A-	-08-914-479	US-09-470-124-55	
3780	19,	3773,	761,		Sequence 58247, A			٠.	4,		415		1,	۳,	4,	2	'n	e 2,	4, 1	3, 2	7, 1	e 57,	57,	5	е 6,	w	26,	26,	quence 10,	5, 2	equence 22,	18,	15,	2	2	Sequence 55, Appl	Sequence 55, Appl

ALIGNMENTS

RESULT 1 US-09-786-648-4

: Sequence 4, Application US/09786648
; GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacc
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438

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Qγ
                                                                                              US-09-786-648-4
                                                                                                                                                                                                                          SOFTWARE: MS DOS
SEQ ID NO 4
                               Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                             LENGTH: 21
TYPE: PRT
ORGANIZM: E. coli
FEATURE:
LOCATION: 45...65
OTHER INFORMATION: 1
OTHER INFORMATION: h
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
GATFQVEVPGSQHIDSQKKAI 21
                               100.0%; Score 106; ilarity 100.0%; Pred. No. 1 Conservative 0; Mismatche
                                                                                                             isolated or synthetic human variant E. coli
                                  Mismatches
                                                                                                                               EtxB
                               DB 21;
1.3e-10;
es 0;
                                                                                                                               beta4-alpha2 loop fragment derivabl
                                  Indels
                                                             Length
                                                                21;
                                 0
                                 Gaps
                                 0;
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RESULT 3
US-08-782-832-15
; Sequence 15, Applicat
; GENERAL INFORMATION:
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US-08-393-334-2
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Best Local Similarity
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GENERAL INFORMATION:
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ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
""""EM: PC-DOS/MS-DOS
""" PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOOSMOI
APPLICANT: Yacoob,
APPLICANT: Zealey,
APPLICANT: Klein,
                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                          APPLICANT: Haq, Tariq A.

TITLE OF INVENTION: BRODUCTION OF AN ORALLY IMMUNOGENIC
TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLANTS
                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
COUNTRY: U.S..
                                                                                                                                                                                                                                                                                                                                    45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 410-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I REGISTRATION NUMBER: 249 REFERENCE/DOCKET NUMBER:
                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                   1 GATFQVEVPGSQHIDSQKKAI 21
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                                                            Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toronto
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Zealey, Gavin R.
Klein, Michel H.
                                                                         E: Pravel, Hewitt, Kimball & Kri
1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 University Avenue, Suite 701
                                                                                                                                                                              Arntzen, Charles J.
Mason, Hugh S.
Haq, Tariq A.
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                              Hewitt, Kimball & Krieger
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                                                                                                                                                                                                                                                                                                                                                                                                Score 106; DB 7;
Pred. No. 9.8e-10;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 4
US-08-817-906-21
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Best Local Similarity
"~+~hes 21; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/08817906 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                     APPLICATE: 24 COLUMN TRILING DATE: 24 COLUMN TRILING DAVID L. ATTORNEY/AGENT INFORMATION: ATTORNEY FOX, DAVID L. ATTORNEY FOX, DAVID L. ATTORNEY FOX, DAVID L. ATTORNEY FOX PARTICULAR PROPERTY AND ATTORNEY FOX PARTICULAR PROPERTY PARTICULAR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 3617/
SEQUENCE CHARACTERISTICS: LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                           TELECOMMUNICATION INFORMATION: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
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APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,612 REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/782,832
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 24-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U. FILING DATE: 08/04/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GATFQVEVPGSQHIDSQKKAI 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
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Pred. No. 9.8e-10;
Mismatches 0;
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; Sequence 20, Application US/09836433
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Vibrio cholerae US-09-836-433-14
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                                                                                      US-09-836-433-22
                                                                                                         RESULT 7
Sequence 22, Application US/09836433
GENERAL INFORMATION:
APPLICANT: YUKi, YOShikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 116
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
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Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
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TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
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CURRENT FILING DATE: 2001-04-16
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Local Similarity 100.0%;
nes 21; Conservative 0;
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                                                                                                                                                                                                                         100.0%; Score 106; DB 22;
100.0%; Pred. No. 1.1e-09;
tive 0; Mismatches 0;
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Pred. No. 9.8e-10;
; Mismatches 0;
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SEQ ID NO 22
LENGTH: 119
TYPE: PRT
ORGANISM: Synthetic construct
US-09-836-433-22
                                                                        ; LENGTH: 124
; LENGTH: 127
; ORGANISM: Escherichia coli
US-09-470-124-55
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; Sequence 55, Application PC/TUS9930747
; GENERAL INFORMATION:
   APPLICANT: Boyce Thompson Institute for Plant Research at Cor; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 4868/85427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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US-09-470-124-55
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PCT-US99-30747-55
     Query Match
Best Local S
Matches 21
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 55
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Best Local S
Matches 21
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CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 55
LENGTH: 124
                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/09470124 GENERAL INFORMATION:
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                                                                                                                                                                                                                           TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed TITLE OF INVENTION: Transgenic Plants FILE REFERENCE: 4868/84454
                                                                                                                                                                                                                                                                                     APPLICANT: Mason APPLICANT: Arntzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-04-16 NUMBER OF SEQ ID NOS: 49
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Local 5.
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les 21; Conserv
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                       Similarity
       Conservative
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     100.0%; Score 106; DB 18; 100.0%; Pred. No. 1.2e-09; Live 0; Mismatches 0;
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                                      Length
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APPLICANT: Dale, James B.

APPLICANT: Dale, James B.

TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER

TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE

FILE REFERENCE: 481112.404C2

CURRENT FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: US/08/914,479

CURRENT FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 08/409,270

PRIOR FILING DATE: 1995-03-23

PRIOR APPLICATION NUMBER: 07/945,860

PRIOR FILING DATE: 1992-09-16

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0
RESULT 12
US-09-756-983-15
; Sequence 15, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
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                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: LT-B-M24 hybrid molecule US-08-914-479A-2
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US-08-914-479-2
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APPLICANT: Dale, James B.
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Best Local Similarity
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LENGTH: 138
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE FILE REFERENCE: 481112.404C2

CURRENT APPLICATION NUMBER: US/08/914,479A

CURRENT FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 08/409,270

PRIOR FILING DATE: 1995-03-23

PRIOR PILICATION NUMBER: 07/945,860

PRIOR FILING DATE: 1992-09-16

NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 1.4e-09;
; Mismatches 0;
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Pred. No. 1.4e-09;
; Mismatches 0;
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RESULT 13
US-09-756-983-18
US-09-756-983-18
; Sequence 18, Application US/09756983
; GENERAL INFORMATION:
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LENGTH: 351
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LENGTH: 313
                                                                                  Matches
                                                                                                                       Query Match
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TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
FILE REFERENCE: 246/285-CIP
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/756,983
CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: 09/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEO ID NOS: 24
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CURRENT FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/105,018
                                                                                                                                                                                OTHER INFORMATION: Fusion constructs with human and bacterial sequences
                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                  TYPE: PRT
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293 GATFQVEVPGSQHIDSQKKAI
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                   1 GATFQVEVPGSQHIDSQKKAI 21
                                                                              Local Similarity
les 21; Conserv
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nes 21; Conserv
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Pred. No. 4.6e-09;
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Pred. No. 4e-09;
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RESULT 14
US-09-756-983-22
; Sequence 22, Application US/09756983
; GENERAL INFORMATION:

APPLICANT: Albani, Salvatore TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,

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Sequence 5, Application US/09786648

Sequence 5, Application:

APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 5
LENGTH: 21
TYPE: PRT
ORGANISM: E. Coli
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Best Local Similarity
Watches 21; Conserve
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; OTHER INFORMATION: Fusion constructs with human and bacterial sequences
US-09-756-983-22
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US-09-786-648-5
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Search completed: October 24, 2002, 15:30:57 Job time: 142.836 secs
                                                                                      밁
                                                                                                                                                                                                                                                            ; LOCATION: 45...65; OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable; OTHER INFORMATION: porcine E. coli US-09-786-648-5
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CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 09/421,506
PRIOR APPLICATION NUMBER: 09/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
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SEQ ID NO 22
LENCTH: 364
TYPE: PRT
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Best Local Similarity
Matches 20; Conserv
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US-10-110-364-17

US-09-791-537-3608

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US-09-791-537-92185

US-09-791-537-94644

US-09-791-537-103241

US-09-791-537-103660

US-10-110-364-2

US-10-110-364-11

US-10-110-364-15

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Sequence 38611, A
Sequence 38639, A
Sequence 74385, A
Sequence 10, Appl
Sequence 13, Appl
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99772, A
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40552, A
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PCT-US02-20978-1	US-10-110-364-9	US-10-110-364-4	US-09-791-537-123948	US-10-110-364-5	US-09-791-537-129309	US-10-110-364-7	US-09-791-537-42610	US-09-791-537-33623	US-10-110-364-8	US-09-791-537-68591	US-10-110-364-23	US-10-110-364-18	US-10-110-364-16	US-09-791-537-60743	US-09-791-537-29489	US-09-791-537-28360	US-10-110-364-20	US-10-110-364-22
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
1, Appl	 Appl 	4, Appl:	123948,	5, Appl:	129309,	7, Appli	42610, 2	33623, 1	8, Appl:	68591, 1	-	18, Appl	16, Appl	60743, 1	29489,	28360, 2	•	22, App.

ALIGNMENTS

US-09-791-537-19387

Sequence 19387, Appl GENERAL INFORMATION:

Application US/09791537

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RESULT 1

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RESULT 2
US-09-791-537-38611
Sequence 38611, Application US/09791537
GENERAL INFORMATION:
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US-09-791-537-19387
; ORGANISM: pdb 1CHPD US-09-791-537-38611
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                                                                          APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICATION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 38611
FENCH. 103
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PAtentIn version 3.0
SEQ ID NO 19387
LENGTH: 103
TYPE: PRT
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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TYPE: PRT
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Pred. No. 2.4e-10;
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APPLICANT: Bionomix, Inc., APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
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US-09-791-537-74385
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                                                                US-10-110-364-10
                                                                                  RESULT 5
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          Sequence 10, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 74385
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Best Local Similarity 100.
Matches 21; Conservative
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 38639
APPLICANT:
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NAME/KEY: VARIANT; LOCATION: (1)...(103); LOCATION: (1)...(103); OTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511 US-10-110-364-10
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US-10-110-364-13
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                                                               Query Match
Best Local Similarity 100.
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 103
TYPE: PRT
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Best Local Similarity 100.0%;
Matches 21; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILLING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
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TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                             FEATURE: WARIANT NAME/KEY: VARIANT LOCATION: (1)...(103) LOCATION: (1)...(103) OTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235 OTHER INFORMATION: (Ogawa 41 R35D).
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Vibrio cholera FEATURE:
                                                                                                                                                                                                                                                                                                          ORGANISM: Vibrio cholera
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45 GATFQVEVPGSQHIDSQKKAI 65
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                                        1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                        100.0%;
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                                                                                                      Score 106; DB 6; Pred. No. 2.4e-10;
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Pred. No. 2.4e-10;
, Mismatches 0;
                                                                                    Mismatches
                                                                                    0
                                                                                                                             Length 103;
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RESULT 7
US-09-791-537-87980
S-09-791-537-87980
Sequence 87980, Application US/09791537
GENERAL INFORMATION:

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US-09-791-537-99772
                                                                                                                                                                           Sequence 12, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 99772
LENGTH: 104
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SEQ ID NO 87980
LENCTH: 104
TYPE: PRT
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Best Local S
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPILICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09-22
NUMBER OF SEQ ID NOS: 153055
                                                    CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Wi
SEQ ID NO 12
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                       Windows Version
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No. 2.4e-10;
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(105)
; OTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa ; OTHER INFORMATION: 41).
US-10-110-364-12
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US-10-110-364-17
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US-09-791-537-73608
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 73608
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Matches
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                                                                                                                 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                            TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A CURRENT APPLICATION NUMBER: US/10/110,364 CURRENT FILLING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
                                                                                                                                   PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                            LENGTH: 12
TYPE: PRT
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                                      ORGANISM: Escherichia FEATURE:
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NAME/KEY: VARIANT
LOCATION: (1)...(123)
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Ewalt, Karla L.
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Pred. No. 2.6e-10;
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LTB variant from NCBI gene bank GI: 1395122

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RESULT 14
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US-09-791-537-78640
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; ORGANISM: Vibrio cholerae
US-09-791-537-40552
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Best Local
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEC ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                              ORGANISM: Vibrio cholerae
                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                              ENGTH: 124
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                                                                                    66 GATFQVEVPGSQHIDSQKKAI 86
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         Application US/09791537
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Pred. No. 2.9e-10;
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 94644
                                                                                                                                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 261/210
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SUMMARIES

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	Nature 288, 499-501, 1980 A;Title: Amino acid sequence homology between cholera toxin and Escherichia coli heat	toxin and Escherichia coli heat
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•	A; Residues: 1-124 < DAL> R; Yamamoto, T.; Gojobori, T.; Yokota, T.	
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ypothetical prote	A;Cross-references: GB:MI/8/4; NID:G14583U; FIDN:AAAS A;Experimental source: plasmid ENT-R PCG86	8064.1; PID:G145831
robable peptide c	R;Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189-10194, 1987	
ensory transducti	A; Title: A functional interaction between the signal	signal peptide and the translation appar
inesin heavy chai	A; Reference number: I41287; MUID:87280041	
horismate synthas	A; Status: preliminary; translated from GB/EMBL/DDBJ	
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tress-activated p nner membrane pro	A;Cross-references: GB:M17101; NID:g146375; PIDN:AAAA R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama	3973.1; PID:g146376 , A.
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rotein 80495.8 [i	A;Cross-reterences: GB:S60/31; NID:g408994; PIDN:AAC00441.1; PID:g408996 R;Tsu]i, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.;	0441.1; P1D:g4U8996 ama, M.; Sakurai, J.; Wada, K.;
	Microb. Pathog. 2, 381-390, 1987	

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A;Accession: S39241
A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-124 <LEW>
A;Cross references: EMBL:X76391; NID:9433859; PIDN:CAA53976.1; PID:9433861
A;Cross references: EMBL:X76391; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I
R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cl
                                                                                                                                                                                                                                                A;Experimental source: gB:AE004224; gB:AE003852; NID:g9655952; R;Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J. Chinese Biochem. J. 9, 395-399, 1993
A;Title: Nucleotide sequence analysis of the gene encoding the company of the service o
                                             A;Molecule type: DNA
A;Residues: 1-20,'Q',22-31,'Q',33-38,'H',40-49,'G',51-67,'T',69-124
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R; Lebens, M.; Holmgren, J.
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A;Accession: A61475
A;Mclecule type: protein
A;Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124 <TSU>A;Experimental source: strain 240-3
C;Complex: the heat-labile enterotoxin molecule contains one A chain and five or s
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A; Residues: 1-124 <LEB>
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A. Molecule type: protein
A. Molecule type: protein
A. Rolecules: 22-38, 'H', 40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
A. Residues: 22-38, 'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
R. R. Rakao, T., Watanabe, H.; Shimonishi, Y.
Eur. J. Biochem. 146, 503-508, 1985
A. Title: Facile identification of protein sequences by mass spectrometry.
A. Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Mitle: Determination of the primary structure A; Reference number: A38033; MUID:78005536
A; Accession: A38033
A; Molecule
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A; Residues: 1-32,'S', 34-74,'S',76-124 <MEK>
A; Cross-references: GB:X00171; NID:g48347; PIDN:CAA24996.1;
R; Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain of cholera en A; Title: Covalent structure of the beta chain of cholera en A; Reference number: A01819; MUID:78005537
A; Accession: A01819
A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124
                                                                                                                                                                                                                                              A; Description: involved in binding of the toxin C; Superfamily: cholera enterotoxin beta chain C; Keywords: enterotoxin; toxin
                                                                                                                                                                                                                                                                                                                                A;Map position: 1
C;Complex: the cholera enterotoxin molecule contains
C;Complex: the with the subunit B, an aggregate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Molecule type: protein 2, A: Residues: 22-38, H', 40-42, 'N', 44-67, 'T', 69-90, A: Experimental source: biotype Inaba 569B A: Note: Asn-65 was partially deaminated to Asp C: Comment: The authors translated the codon TCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 22-38, 'H', 40-42, 'N', 44-67, 'T', 69, 'E', 71-90, 'N', 92-124
A; Note: the difference at residue 70 may be due to deamidation dur
R; Nakashima, Y; Napiorkowski, P; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
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A; Title:
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A;Cross·references: EMBL:X58785; NID:g48888; P
R;Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci.
A;Title: B subunit of cholera toxin produced i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A21910; A; Accession: A21910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Primary structure of the B subunit of cholera enterotoxin A;Reference number: A38034; MUID:77026365 A;Accession: A38034
                                                                                                                                                                                                 F;1-21/Domain: signal sequence *status predicted <SIG>F;22-124/Product: cholera enterotoxin chain B *status
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A; Residues: 1-38, 'H'
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Best Local
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Nucleotide sequence analysis of the
nce number: S17665; MUID:91355224
GATFQVEVPGSQHIDSQKKAI
                                                                            . Similarity
20; Conserv
                                                                                                                                                                            bonds:
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Pred. No. 4.3e-09;
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R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liv
                                                                                                      hypothetical protein T17H3.2 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: C86400
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A; Introns: 44/2; 9
C; Superfamily: Cae
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C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin
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Plant Mol. Biol. 34, 557-562, 1997
A;Title: Characterization and expression of
A;Reference number: 208695; MUID:97369378
A;Accession: T04150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAD23 protein homolog - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04150
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A; Residues: 1-374 <WIL>
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A; Accession: T19866
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A; Residues: 1-392 <SCH>
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Caenorhabditis
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   Jenkins, J.;
Lin, X.; Liu,
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                                                                   C.J.; Federspiel, N.A. Conway, A.B.; Conway,
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Johnson-Hopson, C.; Khan, S.X.; Liu, Z.A.; Luros, J.
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R.; Creasy, T.H.; Dev
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 Khaykin, E.;
Maiti, R.; Ma
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 Marziali,
                                                                      Dewar,
                                                                     Alonso,
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Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
A;Title: Complete genome sequence of a multiple (
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A;Cross-references:
C;Genetics:
A;Gene: STY2026
                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-650 <PAI
                                                                                                                                                                                                                                          C; Accession: AG0733
R; Parkhill, J.; Dougan, G.; Jan
th, T.; Connerton, P.; Cronin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-374 <TET>
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein TC0328 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: D81715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                      A; Reference number: A; Accession: AG0733
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A;Accession: D81715
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A; Residues: 1-574 <STO>
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Gene: TC0328
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                                        GB:AL513382;
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Cronin, A.;
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58.8%;
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                                                                                                                                                           g; Simmonds, M.; Skelton, J.; Stevens
drug resistant Salmonella enterica
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                                      PID:g16503066; GSPDB:GN00176
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A;Cross-references: GB:A;Cross-references: GB:A;C;Genetics:
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Accession: C96580
Query Match
Best Local Similarity
""+"hes 8; Conserve
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                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-255 <S
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A; Residues: 1-91 <STO>
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37.5%;
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                                                Score 44; DB Pred. No. 16;
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Maiti, R.; M
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Maiti, R.; Ma
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war, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                        C;Geneti
A;Gene:
  C;Date: 17-Mar-2000 #sequence_revision C;Accession: T46898; T46899
                                              queuine tRNA-ribosyltransferase N;Alternate names: tRNA guanine C;Species: Zymomonas mobilis
                                                                                                                        T46898
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                                                                                                                                                  RESULT 12
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C:Species: Synechocystis sp.
A; Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_rev.
C:Accession: S76110
R; Kaneko, T: Sato, S.; Kotani, H
o, K.; Okumura, S.; Shimpo, S.; Ti
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: """

A;Molecule type: DNA
A;Residues: 1-1742 <KAN>
A;Cross-references: EMBL:D63999; GB:AB001339;
A;Cross-references: EMBL:D63999; GB:AB001339;
                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-365 <MTH>
A;Cross-references: GB:AE000872; GB:AE000666; NID:g2622082; PIDN:AAB85482.1; PID:g262
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                              R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: S74322; MUID:97061201
A;Accession: S76110
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of
                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: H69231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: H69231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                           A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sensory transduction histidine kinase - Methanobacterium thermoautotrophicum
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Best Local
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                                                                                                                                                                     MTH985
                      ATFQVEVPGSQHIDSQKKA 20
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AIFLVKIPGGELVDANRSA
                                                                                 Similarity 7; Conser
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8; Conser
                                                                                 Conservative
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                                                                                                   40.6%;
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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Pred. No. 1.2e+02;
Pred. No. 1.2e+02;
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Pred.
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                                                                                                   No.
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34;
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                                                                                                                       2
                                                                                                                                                                                                                                                                                             shown;
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(EC 2.4.2.29) [validated] - transglycosylase

Zymomonas

17-Mar-2000

#text_change

18-Aug-2000

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A;Status r. ...
A;Nolecule type: DNA
A;Residues: 1-439 <RIE>
A;Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.110
A;Cross-references: cultivar Columbia; BAC clone MAA21
                                                                                                                                                             RESULT 14
AE2469
R;Kaneko, T.; Nakamura, Y.; Wolk, Nakazaki, N.; Shimpo, S.; Sugimot DNA Res. 8, 205-213, 2001
                                                                          two-component hybrid sensor and regulator all5309 [imported] - Anabaena sp. (strain C;Species: Anabaena sp. (strain PCC 7120) A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
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Best Local Similarity
Thes 8; Conserve
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A; Introns: 39/3; 74/1; 97/3; 138/3; 147/2; 193/3; 200/2; 273/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinesin heavy chain-like protein - Arabidopsis thaliana
N;Alternate names: protein MAA21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Reuter, K.; Ricner, R.
J. Bacteriol. 177, 5284-5288, 1995
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A; Accession: T49189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Complex: monomer [validated, MUID: 95394847]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 5-399 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
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A;Accession: T46899
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A;Molecule type: DNA
A;Residues: 1-399 <REU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence analysis and overexpression of the Zymomonas mobilis tgt gene encoding A;Reference number: Z24129; MUID:95394847
A;Accession: T46898
                                                            C; Accession: AE2469
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: ATSP: MAA21.110
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                    Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
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                                                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
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Pred. No.
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abase, April 2000
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41;
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37;
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                                                                        n or Nostoc sp. strain PCC
#text_change 11-Jan-2002
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Search completed: October 24, Job time: 19.1803 secs

2002, 15:23:22

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A; Dictus: France: DNA
A; Molecule type: DNA
A; Residues: 1-935 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB77008.1; PID:g17134448; GSPDB:GN00179
A; Cross-references: Strain PCC 7120
                                                                                                                                                      C;Superfamily: chorismate synthase
C;Keywords: phosphorus-oxygen lyase; tra
F;347-363/Domain: transmembrane #status
                                                                                                                                                                                                                                                                             A; Accession. 1.7376 A; Molecule type: DNA A; Residues: 1-376 A; Molecule type: DNA A; Residues: 1-376 A; Cross-references: EMBL: Z72670; NID: g1322731; PIDN: CAA96860.1; A; Cross-references: EMBL: Z72670; NID: g1322731; PIDN: CAA96860.1;
                                                                                                                                                                                                                                                                                                                                                                            submitted to the Protein Sequence Database,
A;Reference number: S64153
A;Accession: S64162
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-376 < JON>
A; Residues: 1-376 < JON>
A; Cross-references: EMBL: X60190; NID: g3386; PIDN: CAA42745.1;
R; Volckaert, G; Voet, M; Verhasselt, P; Defoor, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Jones, D.G.L.; Reusser, U; Braus, G.H. Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterizat A;Reference number: S17246; MUID:92114793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces cerevisiae) W.Alternate names: protein G2501; protein YGL148w C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-C;Accession: S17246; S64162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE3469 A;Status; preliminary
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an email to license@isb-sib.ch).
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MEDLINE-95349400; PubMed-7623669;
Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
Todentification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.";
Mol. Microbiol. 15:1165-1167(1995).
-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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ProDom;
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MEDLLNE=91338966; PubMed=2034287;
Sixma T.K. Pronk S.E., Kalk K.H., Wartna E.S., van
Witholt B., Hol W.G.J.;
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J. Mol. Biol. 230:890-918(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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STRAIN-ISOLATE PCG86;
                             Enterotoxin;
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"A functional interaction
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B26946; (
B26946; (
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                                                               1HTL; 20-APR-95.
PPO; IPRO01835; Enterotoxin_B; 1.
PP01376; Enterotoxin_B; 1.
S; PR00772; ENTEROTOXINB.
m; PD012805; Enterotoxin_B; 1.
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03-DEC-97
03-DEC-97
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Best Local Similarity 95.3
Matches 20; Conservative
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SEQUENCE FROM N.A.
STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
MEDLINE-84068199; PubMed-6646234;
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P01556; Q9JQO2;
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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             SEQUENCE FROM N.A. STRAIN-1854 / O139-BENGAL; Yamamoto K., Do V.G.R.F., Honda T.;
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Nucleotide sequence analysis of the
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MEDLINE=94237453; PubMed=8181723;
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Nature 306:551-557(1983).
[3]
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MEDLINE=84061784; Pubmed=6315707
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Bacteria; Proteobacteria;
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                                 Albert
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                                                                                                                                  Vibrio
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EMBL; EMBL; EMBL; EMBL; EMBL;

XVVCB

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[6]
SEQUENCE FROM N.A.
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STRAIN-EL TOR N16961 / SEROTYPE 01;
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLING-2040683; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nicardson D.,
Gill S.R., Nelson K.E., Read T.D., Bass S., Qin H., Dragoi I., Sellers P.
Ermolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P.
Ermonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
"-~~nald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
"-~~nald L., Utterback T., Colwell R.R., Mekalanos J.J., Venter J.C.
                                                                                                                                                                                                                                                 "Structural studies of receptor binding by cholera toxin mutants.";
Protein Sci. 6:1516-1528(1997).
-I- FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN
BINDING TO CELL MEMBRANES.
-I- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN
(FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN
DISULTIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO SEED BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO SEED BOND.
                                                                                              EMBL;
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang R.G., Westbrook M.L., Wes
Maulik P.R., Reed R.A., Shipley
"The 2.4 A crystal structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pentasaccharide.";
Protein Sci. 3:166-175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kurosky A., Markel D.E., Peterson J.W "Covalent structure of the beta chain J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                      modified and this statement entities requires a license
                                                                                                                                                                     use
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MEDLINE=95387394; PubMed=7658472;
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MEDLINE=94272319; PubMed=8003954;
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          X00171; CAA24996.1;

K01170; AAA27573.1;

D30053; BAA06291.1;

X58786; CAA41593.1;

X76390; CAA53973.1;

X76391; CAA53976.1;

X76391; CAA53976.1;

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Grafham D.;
Submitted (JUN-1998) to t
-!- SUBCELLULAR LOCATION:
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O14896;
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                                 Grossman
                                                            Eukaryota;
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15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
                                                                                                               HUMAN
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pfam; pF01376; Enterotoxin_B; 1.
pRINTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
                 SEQUENCE FROM N.A.
                            Submitted
                                      SEQUENCE FROM N.A.
                                                  NCBI_TaxID=9606;
                                                       Mammalia; Eutheria;
                                                                             Interferon regulatory
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$114624; $14624.

$2CHB; 03-DEC-97.

$3CHB; 12-AUG-98.

$1CHP; 08-MAR-96.

$1CHP; 08-MAR-96.

$1CHP; 08-MAR-96.

$1CHP; 01-APR-97.

$1XPB; 01-APR-97.

$1XPB; 01-APR-97.

$1XPC; 01-AUG-96.

$1CHP; 15-CCT-97.
                                                                  sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                   VC1456;
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                                                                                                                                                                Similarity
                           A., Mittrucker
d (SEP-1997) to
                                                                                                                                                                                                                                                                                                                         Enterotoxin;
                                                             Metazoa;
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xin; Signal; 3D-s
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                                                             Chordata;
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95.2%;
                                                                             Last sequence update)
Last annotation update)
factor 6 (IRF-6).
                                                                                              Created)
the EMBL/
N: Nuclear
                           H.W., Antonio L., Ozato K., Mak the EMBL/GenBank/DDBJ databases
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     EMBL/GenBank/DDBJ databases
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Pred. No.
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                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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01-MAR-2002 (Rel. 41, C
01-MAR-2002 (Rel. 41, I
01-MAR-2002 (Rel. 41, I
                                                                                                      MGD; MGI:1859211; Irf6.
InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 467 AA; 53106 MW; 68CCAA90680FEDC8 CRC64;
                                             PRINTS; PR00267; INTERNREGECT.
PRODOMS; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               Grossman A., Mittrucker H.W., Antonio L., Mak Submitted (OCT-1996) to the EMBL/GenBank/DDBJ-i-SUBCELLULAR LOCATION: Nuclear (Potential).
-:- SIMILARITY: BELONGS TO THE IRF FAMILY.
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PRINTS; PR00260; INTERNREGECT.
PRODOM; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
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                                                                                                                                                          HSSP; P23906;
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                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
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factor 6 (IRF-6).
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01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Queuine tRNA-ribosyltransferase (EC 2.4.2.29)
                                                                                                                                                                                                                                Graedler U., Gerber H.-D., Goodenough-Lashua D.M., Garcia G.A., Ficner R., Reuter K., Stubbs M.T., Klebe G.;
"A new target for shigellosis: rational design and crystallographic studies of inhibitors of tRNA-guanine transglycosylase.";
J. Mol. Biol. 306:455-467(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A.
STRAIN-ATCC 31821 / ZM4 / CP4;
MEDLINE-92406015; PubMed=1526462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis and overexpression of the gene encoding tRNA-guanine transglycosylase: biochemical characterization of the enzyme.";
J. Bacteriol. 177:5284-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96256303; PubMed=8654383; Romier C., Reuter K., Suck D., Ficner R.; Trystal structure of tRNA-guanine transglycosylase: RNA modification by base exchange.";
                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                           EMBO J. 15:2850-2857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEMS Microbiol. Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and molecular characterization from Zymomonas mobilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shark K.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reuter K.K.H., Ficner R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SEQUENCE OF 1-6, MEDLINE-95394847; PubMed=7665516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zymomonas
               between
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                                                                  MAGNESIUM.
SUBUNIT: MONOMER.
SIMILARITY: BELON
CAUTION: REF.2 SE
                                                                                                                                              FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAS with GU(N) anticodons (tRNA-Asp, -Asn, and -Tyr). After this exchange, a cyclopentendiol molety is attached to the 7-aminomethyl group of 7-deazaguanine, result: in the hypermodified nucleoside queuosine (Q) (7-((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine). CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
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                                                                                                                      guanine.
COFACTOR: BINDS
                                                       To
              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVEVPGSQHIDSQKKAI
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                                                                 TY: BELONGS
REF.2 SEQUE
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 Swiss Institute
Bioinformatics
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                                                                  SEQUENCE
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                                                                                                                       REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES
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                                                                 THE QUEUINE TRNA-RIBOSYLTRANSFERASE I
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STRAIN=S288C / FY1769;
MEDLINE=97197983; PubMed=9046099;
MEDLINE=97197983; PubMed=9046099;
MEDLINE=971979983; PubMed=9046099;
MEDLINE=97197983; PubMed=9046099;
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P28777;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Chorismate synthase (EC 4.6.1.4) (5-enolpyruvylshikimate-3-phosphate
Chorismate + phosphate.
-!- COFACTOR: REDUCED FLAVIN.
-!- PATHMAY: SEVENTH STEP IN THE BIOSYNTHE
THE BIOSYNTHESIS OF AROMATIC AMINO ACI
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92114793; PubMed-1837329;
Jones D.G.L., Reusser U., Braus G.H.;
Jones D.G.L., Reusser U., Braus G.H.;
Molecular cloning, characterization and analysis of the regulation
of the ARO2 gene, encoding chorismate synthase, of Saccharomyces
cerevisiae.";
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pfam; PF01702; TGT; 1.
Queuosine biosynthesis; Transferase; Glycosyltransferase;
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                                                                                                                                                    1, MRF1 genes and six new open reading frames.";
st 13:177-182(1997).
CATALYTIC ACTIVITY: 5-0-(1-carboxyvinyl)-3-phosphoshikimate
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L33777; AAA27705.1; ALT_INIT.
Z11910; -; NOT_ANNOTATED_CDS.
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ST14_H
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                                                                                                                                                                                                     Takeuchi T., Shuman M.A., Craix c.s.,
Takeuchi T., Shuman M.A., Craix c.s.,
"Reverse biochemistry: Use of macromolecular protease inhibitors a
dissect complex biological processes and identify a membrane-type
serine protease in epithelial cancer and normal tissue.";
serine protease in epithelial cancer and normal tissue.";
hard Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-99432178; PubMed-10500122;
Takeuchl T., Shuman M.A., Craik C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-99303581; PubMed-10373424;

Lin C.Y., Anders J., Johnson M., Sang Q.A.,

"Molecular cloning of cDNA for matriptase,
protease with trypsin-like activity.";

J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15 (Tumor associated differentially-expressed gene-15 protein).
ST14 OR PRSS14 OR SNC19 OR TADG15.
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InterPro; IPR000453; Chorismate_Synt; 1.
Pfam; PF01264; Chorismate_Synt; 1.
ProDom; PD002941; Chorismate_Synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid biosynthesis.
SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                  Yamaguchi N., Mitsui S
"Molecular cloning of
SEQUENCE
                                                 Submitted
                                                                                                                                                    TISSUE-Prostate;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
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SIMILARITY:
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S0003116; ARO2.
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X99960; CAA68214.1; -.
Z72670; CAA96860.1; -.
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Q9H3S0; Q9HCA3; Q9BSO1; Q9HB36;
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Pred. No. 17
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; Homo.
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMB
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CUB 1.
CUB 2.

(TYPE-II MEMBRANE

PROTEIN)

TRANSMEM DOMAIN

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PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA_1; 2
PROSITE; PS50068; LDLRA_2; 4
PROSITE; PS50240; TRYPSIN_DO
PROSITE; PS00134; TRYPSIN_HI
PROSITE; PS00135; TRYPSIN_SE
                                                                                                                                                                                                                                                            Interpro; IPR000859; (Interpro; IPR001314; (Interpro; IPR002172; Interpro; IPR001254; Interpro; IPR001254;
                                                                                                                                                                         SMART;
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PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00042; CUB; 2.
SMART; SM00192; LDLa; 3.
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"Genomic analysis of a novel
                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                   Fransmembrane;
                                                                                Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 C.Y., Anders J., Johnson M., Dickson R.B.;
1 Initication and characterization of a complex containing matriptase
2 a Kunitz-type serine protease inhibitor from human milk.";
2 biol. Chem. 274:18237-18242(1999).
2 FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE
2 IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE
2 ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUBSTRATES WITH ARG
3 OR LYS AS THE P1 SITE.
3 SUBCELLULAR LOCATION: Type II membrane protein (Probable).
3 SIMILARITY: CONTAINS 2 CUB DOMAINS.
3 SIMILARITY: CONTAINS 2 CUB DOMAINS.
3 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
3 TRYPSIN TAMELY.
                                                                                                                                                                                                                                                                                                                                ; AF118224; AAD42765.2; AF13086; AAF00109 1; AB030036; BAB20376.1; AF057145; AAG15395.1; AF283256; AAG13949.1; AF283256; AAG13949.1;
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PF00057; ldl_recept_a; 4.
PF00089; trypsin; 1.
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                                                                     Repeat
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Tryp_SPc;
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TRYPSIN_HIS;
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RESULT 9
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Best Local
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ACT_SITE
                              "4-aminobutyrate aminotransferase (GABA-transaminase)
J. Inherit. Metab. Dis. 22:414-427(1999).
-i- CATALYTIC ACTIVITY: 4-aminobutanoate + 2-oxoglutasenialdehyde + L-glutamate.
-i- COPACTOR: PYRIDOXAL PHOSPHATE.
-i- SUBGUNIT: MONOMER (PROBABLE).
-i- SUBCELLGUAR LOCATION: MITOChondrial matrix.
-i- TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KII
                                                                                                                                                                                                                                                                                                                                                                                                 4-aminobutyrate aminotransferase, mitochondrial precursor (EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT).

ABAT OR GABAT.
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CARBOHYD
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DOMAIN
                                                                                                                     MEDLINE-99336116; PubMed-10407778; Medina-Kauwe L.K., Tobin A.J., De Nyhan W.L., Gibson K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                                                                                 de Biase D., Barra D., Simmaco M., John R., "Primary structure and tissue distribution
                                                                                                                                                                                                                                                                  "Screening and sequence determination c
brain 4-aminobutyrate aminotransferase.
Gene 155:185-187(1995).
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                           Eur. J. Biochem.
                                                                                                                                                                                         aminotransferase.
                                                                                                                                                                                                                                             SEQUENCE OF 368-465 FROM N.A.,
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                                                                                                                                                          VARIANT LYS-220
                                                                                                                                                                                                                       MEDLINE=95154329; PubMed=7851425;
                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                                                                                                                                                                                                                                                              MEDLINE=95237607; PubMed=7721088;
                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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           PLACENTA.
DISEASE: DEFECTS IN
  PHENOTYPE INCLUDES
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                                                                                                                                                                            227:476-480(1995).
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                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%;
N ABAT ARE A CAUSE OF GABA-AT DEFICED PSYCHOMOTOR RETARDATION, HYPOTONIA,
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Catarrhini;
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-> V (IN REF. 3).
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                                                                                                                                  Meirleir
            CAUSE OF GABA-AT DEFICIENCY WHOSE
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RELAY SYSTEM
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GTR (IN REF. 5).
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human
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RESULT 10
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Best Local
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01-MAR-2002
Pullulanase
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P07206;
01-APR-1988
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VARIANT
                                                   STRAIN=UNF 5023;
MEDLINE=90205629; PubMed=2181242;
Kornacker M.G., Pugsley A.P.;
"Molecular characterization of pulA and its secreted enzyme of Klabsiella pneumoniae UNF Mol. Microbiol. 4:73-85(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L32961; AAA74449.1;
HSSP; P80147; 1GTX.
MIM; 137150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 1-62 FROM N.A MEDLINE=86033621; PubMed=
                                                                                                                                                                                                                      Bacteria; Proteobacteria; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
Transferase; Aminotransferase; Pyridoxal
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                                                                                                                                                                                                                                                        Klebsiella
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                                                                                                                                                                                                 NCBI_TaxID=573;
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ABNORMALITIES.
SIMILARITY: BELONGS
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(Rel. 14, L)
(Rel. 41, L)
(Rel. 41, L)
precursor ()
(Pullulan)
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 PubMed=3902792;
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Last annotation update)
(EC 3.2.1.41) (Alpha-dextrin
n 6-glucanohydrolase).
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Pred. No. 34;
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                                                                      UNF5023.";
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EMBL; M12503; F
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ACT_S:
ACT_S:
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"Structure of two divergent promote encoding pullulanase in Klebsiella regulated by the malT product.";
D. Bacteriol. 164:639-645(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Klabsiella pneumoniae puls gene encodes an outer membrane lipopprotein required for pullulanase secretion.";

J. Bacteriol. 171:3673-3679(1989).

-i- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic linkages in pullulan and in amylopectin and glycogen, and the alpha-and beta-limit dextrins of amylopectin and glycogen.

-i- SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02922; isoamylase_N; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00128; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A25025; A25025.
PIR; A32880; A32880.
PIR; S31823; S31823.
InterPro; IPR000461; Alpha_amylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                         1 GATFQVEVPGSQHID-----SQKKAI 21
                                                                                                                                                                                                                   Match
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SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                               GVTFRVWAPTAQQVDVVVYSADKKVI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                     Similarity 38.1
10; Conservative
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; CAA36431.1; -.
; AAA25087.2; -.
; AAA61976.1; -.
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                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane;
 sequence up
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N-ACYL DIGLYCBRIDE.
BY SIMILARITY.
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C (IN REF. 2).
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T -> MATA (IN REF. 2).
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bsigla pneumoniae and positively
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Pred.
                                                           PRT;
                                                                                                                                                                                       Mismatches
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No. 78;
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-> MATA (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein;
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on update)
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use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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or send an
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                                                                                      the
                                                                                                          between
                                                                                                                                                                                                                   <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                             Westphal M., Mueller-Tauben
"Transcript regulation and
Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 13-76
STRAIN-AX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-87257921; I Giorda R., Ennis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminal tail and antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1)
SEQUENCE FROM N.A.
MEDLINE=88152253; PubMed=2831095;
MEDLINE=88152253; PubMed=2831095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ubiquitin.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structure of two developmentally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete cDNA sequence of a Dicterminal tail and identification
                                                                                                                                                             REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME BIOGENESIS.
SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                              S Lett. 209:92-96(1 FUNCTION: INVOLVED CELLULAR PROTEINS,
                                                                                  European
                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation surpean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
  email to license@isb-sib
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                                                                                                                                                                                                                                                                                                                                                                                 Mueller-Taubenberg A., Noegel regulation and carboxyterminal
                                                                                                                                                                                                                                                                          INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE N OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=3037345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eum (Slime mold)
Dictyosteliida;
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tion of the pro
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                                        Usage
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of ubiquitin
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EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; ;; X07210; CAA30183.1 ;; M19666; AAA33261.1 ;; M19491; AAA33267.1 ;; M23748; AAA33262.1 ;; M23748; AAA33263.1 ;; M23750; AAA33264.1 ;; M23751; AAA33265.1 ;; M23751; AAA33265.1 ;; M23752; AAA33266.1 ;; M23753; AAA33266.1 ;; M23754; AAA33268.1 ;; M23754; AAA33268.1 CAA30183.1; ALT_TERM.
ALT_TERM. (See http://www.isb-sib.ch/announce/

EMBL; EMBL;

S00357; E34080;

UQDOR. UQDOR7. A27806. B27806. A34080.

A27806; B27806; A34080; B34080; C34080; D34080;

lubi.

EMBL;

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RESULT 12

YP68_CAEEL
ID YP68_C
AC 009217
O1-NOV
DT 01-NOV
DT 01-N
YAAN_BACSU
ID ANAN_B
AC P37535
DT 01-OCT
DT 16-OCT
DE Hypoth
GN YAAN.
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Best Local S
Matches 9
                                             01-OCT-1994
01-OCT-1994
16-OCT-2001
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01-NOV-1997
01-NOV-1997
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VARIANT
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SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
Nuclear protein; Polyprotein.
SITE

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NECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kirsten J.;
Submitted (FEB-1995) t
-!- SIMILARITY: SOME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 37.0 kDa protein B0495.8 in chromosome
                                                                                                                   YAAN_BACSU
P37535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
    Hypothetical YAAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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mes 6; Conserv
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9; Conservative
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                        (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 40, Last annotation updat)
1 43.8 kDa protein in XPAC-ABRB
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` AA;
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                                                                                                                                         STANDARD;
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42.9%;
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TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
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Pred. No.
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CONJUGATION TO ACCEPTOR PROTEINS
K -> N (IN SOME CLONES REPEATS).
6427383968EABA84 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 41;
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5.3;
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                        intergenic region
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 313;
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RESULT PMS2LT PM
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P54278;
01-OCT-1996
01-OCT-1996
16-OCT-2001
Bronner C.E., Baker S.M., Morrison P.T., Warren G., Smit
Lescoe M.K., Kane M., Earibino C., Lipford J., Lindblom
Tannergaard P., Bollag R.J., Godwin A.R., Ward D.C.,
Nordenskjoeld M., Fishel R., Kolodner R.D., Liskay R.M.,
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                              TISSUE-Endometrial tumor;
MEDLINE-94352394; PubMed=8072530;
Micolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K
Ruben S.M., Rosen C.A., Haseltien W.H., Fleischmann R.D.,
Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S
Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.
"Mutations of two PMS homologues in hereditary nonpolyposis c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMS1 protein PMS2 OR PMSL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; CONFLICT 191 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D26185; BAA05262.1; -.
EMBL; M96156; AAA22892.1; -.
EMBL; Z99104; CAB11802.1; -.
SubtiList; BG10090; yaaN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bookstein C., Edwards C.W., Hulett F.M.; Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180\, kilobase region of the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-191 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilis chromosome containing the replication origin.";
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Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                        Nature
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                                                                                                                                                                   371:75-80(1994).
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(Rel.
(Rel.
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, Last sequence update)
, Last annotation update)
2 (DNA mismatch repair protein PMS2).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
-> M (IN REF. 2).
D921F3A0F6845EEE CRC64;
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31;
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                         R.M.;
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                                                                                               Smith
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RESULT 15
HS74_CAPEL
ID HS74_C
AC P20163
DT 01-FEB
DT 15-JUL
DE Heat s
GN HSP-4
OS Caenor
OC Eukary
OC Rhabdi
OX NCBI_T
RN [1]
RP SEQUEN
RX HESCHI
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RL Genome
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Best Local
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89306577; PubMed-2744444;
Heschl M.F.P., Baillie D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
Heat shock 70 kDa protein D (Fragment).
HSP-4 OR HSP70D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U13696; AAA63923.1; -.
EMBL; U14658; AAA50390.1; -.
HSSP; P23367; 1BKN.
SWISS-2DPAGE; P54278; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       Genome 32:190-195(1989)
                                                                                                                                                                                                                                                                                                            elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS74_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002099; DNA_mis_repair.
InterPro; IPR003594; HATPase_c.
Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA repair;
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 600259;
                                                                                                                                                                                                                                                                                                                                  "Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
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                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
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DISEASE: ASSOCIATED WITH FAMILIAL HEREDITARY NONPOLYPOSIS COLON CANCER (HNPCC) (LYNCH SYNDROME). HNPCC IS ONE OF THE MOST COMMON GENETIC DISEASES IN THE WESTERN WORLD, AND ACCOUNTS FOR 15% OF ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                               TO MAMMALIAN GRP78.
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862 AA;
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                                                                                                                                                                                                                                    LOCATION: Endoplasmic reticulum lumen.
BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG
                                                                                                                                                                                                                                                                                                                             of a heat-shock pseudogene
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95797 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis.
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P -> S (IN REF. 2).
; B60A605222CBBCAC CRC64;
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Pred. No. 88;
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Best Local S
Matches
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InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                             PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; PARTIAL.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene
                                                                                                                                                                                                 EMBL; M28528; AAA28076.1; -. HSSP; P19120; 3HSC.
                                                                                                    NON_TER
                                                                                                                                             PROSITE; PS00014; ER_TARGET; PROSITE; PS00297; HSP70_1; PA
                                                                                 SEQUENCE
133 TFEIDVNGILHVSAEDK 149
                    ω
                   TFQVEVPGSQHIDSQKK 19
                                        Similarity 6; Conserv
                                                                                 288 AA;
                                                                                           285
                                        Conservative
                                                                         288
.; 31267 MW;
                                                 37.7%;
                                                                                                                                               PARTIAL
                                         6,
                                                                                PREVENT SECRETION FROM ER 967F5A4A12FA67BF CRC64;
                                                          Score 40;
                                                   Pred.
                                         Mismatches
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Search completed: October 24, Job time: 10.2623 secs 2002, 15:21:03

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Result
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Perfect score:
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Listing first 45 summaries
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sp_phage:*
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sp_mhc:*
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Q9P4E0
Q99876
Q993M9
Q9SXC9
                                                                                                                 Q57193
Q9RP15
Q56635
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Q57193 vibrio chol Q9rp15 vibrio chol Q9rp15 vibrio chol Q5635 vibrio chol Q3v32 escherichia Q94m01 vibrio phag Q9r646 vibrio chol Q91jb0 arabidopsis Q9987 homo sapien Q91gm2 oryza sativ Q40742 oryza sativ Q40742 drosophila Q9p4e0 ustilago ma Q49876 lupinus alb Q9u3m9 caenorhabdi Q9sxc9 arabidopsis Q9pky2 chlamydia m
                                                                                                                                                   Description
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 $\begin{array}{c} 117 \\ 128 \\ 138 \\$

ALIGNMENTS

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Q57193 PRELIMINARY; PRT; 124 AA. Q57193; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                        InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
                                                                                                                                                                            STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993).
                                                                                                                                                                                                                                                       Dams E., De Wolf M., Dierick W.; "Nucleotide sequence analysis of the CT operon classical strain 569B.";
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CLASSICAL STRAIN 569B;
MEDLINE=91355224; PubMed=1883
                                                                                                                                                                                                                                                                                                                                                                                        CTXB
                                                            EMBL; X58785; CAA41591.1;
EMBL; U25679; AAC34728.1;
EMBL; A00931; CAA00098.1;
HSSP; P01556; 2CHB.
                                                                                                               Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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             ProDom;
                                                                                                                                        STRAIN-CLASSICAL BIOTYPE 569B;
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                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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in. Biochem.
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             PD012805;
             Enterotoxin_B;
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CHAIN
SEQUENCE
                                   "Comparison of cholera toxin genes (ctxAB) of non-O1 strains 854 (O139-bengal) and 87 (O37) from two ouths Submitted (APR-1994) to the EMBL/GenBank/DDBJ database EMBL; D30052; BAA06289.1; HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shin H.J., Park Y.C., Kim Y.C.; "Cloning and nucleotide sequence analysis of the cassette from Vibrio cholerae KNIH002 isolated Misainmurhag Hoiji 35:205-210(1999).
EMBL; AF175708; AAD51360.1; -.
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Pfam; PF01376; Enterotoxin_B; 1.

PRINTS; PR00772; ENTEROTOXINB.

PRODOM; PD012805; Enterotoxin_B; 1.

SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9
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Bacteria; Proteobacteria;
NCBI_TaxID=666;
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STRAIN=KNIH002;
Shin H.J., Park Y.C.,
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01-JUN-2001
                                                                                                                                    Honda T.;
                                                                                                                                                    Yamamoto K.,
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ENTEROTOXIN B-SUBUNIT.
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CHOLERA TOXIN B PROTEIN (CTB).
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  BADUENCE FROM N.A.
Bhattacharyyaa T., Nandy R.K.,
The entire core region of the
environmental strain of V. chol
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Viruses; ssDNA viruses;
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Submitted (MAR-1998)
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MEDLINE=95091056; PubMed=7998417;
MEDLINE=95091056; PubMed=7998417;
MEDLINE=95091056; PubMed=7909417;
MEDLINE=1001056; PubMed=1001057; National House PubMe
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llarity 100.0%;
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Pred. No. 2.6e-10;
Mismatches 0;
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Pred. No. 1
Nair G.B.;
ctx-phi (ctx-prophage)
lerae.";
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Best Local
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01-MAY-2000 (TremBLrel. 13
01-MAY-2000 (TremBLrel. 13
01-UN-2001 (TremBLrel. 17
CHOLERA-LIKE ENTEROTOXIN B
                                                                                                                                                                                                                                                                                                                         Q9LJB0;
Q1-QCT-2000 (TrEMBLrel. 1
Q1-QCT-2000 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
EMB|CAB77996.1.
 "Structural analysis of Arabidopsis Sequence features of the regions of TAC and BAC clones.";
                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF414369; AAL09682.1; -. SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
                                                                                          SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LJB0
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ProDom; PD012805; Enterotoxin_B; 1
SEQUENCE 103 AA; 11645 MW; 992
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Nakashima K., Eguchi Y., Nakasone
"Characterization of an enterotox
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                                                      Nakamura Y.;
                                                                       MEDLINE=20363099; PubMed=10907853;
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PF01376; Enterotoxin_B; 1.
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P01556; 1XTC.
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EMBL/GenBank/DDBJ databases
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4,251,695 bp covered
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STRAIN=CV. Sasaki T., I "Oryza sati

NIPPONBARE;
Matsumoto T., Yaman
iva nipponbare(GA3)

Yamamoto

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chromosome

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sativa

SEQUENCE FROM N.A.

Q9LGM2; Q9LGM2; Q1-OCT-2000 01-OCT-2000 01-DEC-2001

(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 19,

Last sequence update)
Last annotation update)

Created)

PRELIMINARY;

PRT;

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ESTS AU056822(S20908).
Oryza sativa (Rice).
Eukaryota; Viridiplantae;

Streptophyta;

Embryophyta;

Tracheophyta;

Poales;

Liliopsida;

Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza, NCBI_TaxID=4530;

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Best Local :
                                                                                          Matches
                                                                                                              Query Match
Best Local
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01-MAY-1997
01-JAN-1998
01-DEC-2001
                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine/threonine-protein kinase; Tr SEQUENCE 508 AA; 58126 MW; 157FBF8F448511AF4
                                                                                                                                                                                                                                                                                                                                                  Genomics 45:327-331(1997).
-!- SIMILARITY: BELONGS TO
EMBL; AB000450; BAA19109.1,
HSSP; Q06486; 1CKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98008921; PubMed=9344656;
Nezu J., Oku A., Jones M.H., Shimane M.;
"Identification of two novel human putative YRK1 and VR K2, with structural similarity t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRK2.
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EMBL; AP000606; BAB01195.1;
SEQUENCE 552 AA; 63036 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
329
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                                       1 GATFQVEVPGSQHIDSQKKA
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GQSINVHTPNSQKVDSQKAA
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                                                                                                                                                                                                                                                                                                                                                                          BELONGS TO BAA19109.1;
                                                                                                           48.1%;
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Last sequence update)
Last annotation updat
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                                                                                        Pred. No. 3.1
2; Mismatches
                                                                                                                                 Score 51;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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2.3;
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to Vaccinia virus
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                                                                                                                                                                                     CRC64;
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RESULT
Q440742
ID Q740742
AC Q4
D7 Q1
D7 Q1
Q7 Q
RESULT
Q9NKD5
ID Q9
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Q9NKD5;
Q9NKD5;
01-OCT-2000
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Q40742;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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Submitted (JUN-:
[2]
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OTYZA SATIVA (Rice).
OTYZA SATIVA (Rice).
EUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530;
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EMBL;
HSSP;
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Submitted (JUN 2000) to the EM
EMBL; AP002521; BAA96762.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 34:557-562(1997).
EMBL; U63530; AAB65841.1; -.
HSSP; P54725; 1DVO.
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Pfam; PF00441; Acyl-CoA_dh.; 1.
Pfam; PF02770; Acyl-CoA_dh_M; 1.
Pfam; PF02771; Acyl-CoA_dh_M; 1.
Pfam; PF02771; Acyl-CoA_dh_N; 1.
PFROSITE; PS00073; ACYL_COA_DH_2;
PROSITERY PS00073; ACYL_COA_DH_2;
PS00073; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schultz T.F., Quatrano R.S.;
"Characterization and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-NIPPONBARE; MEDLINE-97369378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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"Oryza sativa nipponbare(GA3) geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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; SM00213; UBQ;
TE; PS50053; UBI
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9; Conserv
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       (TrEMBLrel.
                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UBIQUITIN_2; ; 41754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9225866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46132 MW;
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Last annotation updat
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Pred. No. 5.6;
2; Mismatches
       Created;
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Pred. No. 7.6;
5; Mismatches
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BD6E08574CC7CACB
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Q9P4E0;
Q1-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-DEC-2001 (TrEMBLrel. 19, L
PHEROMONE-RESPONSIVE MAPKK KI
                                                                                                                            Eukaryota; Fungi; Basidiomycota; Us: Eukaryota; Fungi; Basidiomycota; Us: Ustilaginomycetidae; Ustilaginales; NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                           MEDITINE-20331594; PubMed=10875339;
Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
"The Ustilago maydis ubc4 and ubc5 genes encode members kinase cascade required for filamentous growth.";
Mol. Plant Microbe Interact. 13:781-786(2000).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; AF197562; AAF86841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palazzoto A., Rubin G.M.;
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T. Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelav
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MEDLINE=99403001; PubMed=10471707;
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NCBI_TaxID=7227;
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                    HSSP; P24941;
                                                                                                       STRAIN=1/
                                                                                                                 SEQUENCE
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IPR000719;
IPR000159;
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395 AA; 4
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                    1B38.
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56.2%;
Euk_pkinase
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Pred. No.
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                                                                                                                                              Ustilaginomycetes; es; Ustilaginaceae;
                                                                                                                                                                                                  sequence update) annotation updat
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11;
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                                          PROTEIN
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                                                                                                                                               Ustilago.
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DT 01
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Best Local S
Matches 10
                                Q9U3M9;
Q1-MAY-2000 (TrEMBLrel.:
Q1-MAY-2000 (TrEMBLrel.:
Q1-MAR-2001 (TrEMBLrel.:
C40H5.3 PROTEIN.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                   Pfam; PF00192; chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Glycosidase; Hydrolase; Signal.
SIGNAL 1 27 POTEN
                                                                                                                                                                                                                                                                                                                                                            from Lupinus albus.";
Submitted (FEB-1998) to
-i- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TremBLrel. 06, Created)
01-JUN-1998 (TremBLrel. 06, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
CLASS.III CHITINASE PRECURSOR (EC 3.2.1.14).
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pfam; pF00069; pkinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; pS00107; pROTEIN_KINASE_ATP; 1.
PROSITE; pS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; pS00118; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein
ATP-binding; Kinase; Serine/threonine-protein
SEQUENCE 1166 AA; 123298 MW; A89E0019AABD4
                                                                                                                                                                                                                                                                                                              EMBL; Y16415; CAA76203.1; -. HSSP; P23472; 2HVM. InterPro, IPR001579; Chitinase_2.
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Regalado A.P., Vidal S.,
Rodrigues-Pousada C.;
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Eukaryota; Viridiplantae; Str
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Nematoda; Chromadorea; rinae; Caenorhabditis.
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                                                     Created)
Last sequence update)
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Pred. No. 47;
4; Mismatches
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Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
T17H3.2 PROTEIN (AT1G27520/T17H3_2).
T17H3.2.
                                                                                                                      "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the
EMBL; AC005916; AAAA5990.1;
EMBL; AY056382; AAL08238.1;
HSSP; P32906; 1DL2.
                                                                                                                                                                                                         Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., L

Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sa

Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., B

Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.

Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Wal

Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome I BAC T17H3 sequence.";

Submitted (AUG-1999) to the EMBL/GenBank/DDEJ databases.
                                                                    InterPro; IPR001382; Glyco_hydro_47.
pfam; PF0152; Glyco_hydro_47; 1.
PRINTS; PR00747; GLYHDRLASE47.
ProDom; PD003239; Glyco_hydro_47; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SXC9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9SXC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281482; CAB03954.2; -.
SEQUENCE 374 AA; 42198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. White S.;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                               Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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8; Conserv
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                                                       574 AA;
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                                                       Glyco_hydro_47;
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42.1%;
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Score 46; DB Pred. No. 26; 2; Mismatches
                                                                                                                                                                     EMBL/GenBank/DDBJ
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16;
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                           Length 574;
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, Hayashizaki y
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Matches

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Result
No.
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Listing first 45 summaries
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length: 100
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   Length
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Description
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Arabidonsis thali	4			٠		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAG42341	<u>ی</u>	1		بر م	•
Zea mays prote	AAG18728	21	77	•	38	-
Arabidopsis thali	AAG15994	21	77	•	38	_
Arabidopsis thalia	AAG13297	21	77	•	38	
Arabidopsis thali	AAG06889	21	77	•	38	
Ubiquitin monome	AAY90254	21	76	•	38	
en	AAW60701	19	76	•	38	
idop	AAG33547	21	71	٠	38	
Zea mays protein	AAG40689	21	69	٠	38	
Zea mays protein	AAG32702	21	69	٠	38	
늉	AAU46087	22	57	٠	38	
Peptide #11673	AAM37636	22	51	•	38	
Peptide #7832 enco	39	22	51	•	38	
one n	AAM77476	22	51	•	38	
Human brain expre	AAM64700	22	51	•	38	
Protein #8680 enco	ABB26681	22	51	•	38	
	ABB43738	22	51	•	38	
Human polypept	AA012358	22	48	35.5	38	
Yeast ubiquitin	AAB03161	21	76	•	39	
Ubiquitin compone	AAW41801	19	76	36.4	39	
	AAR85462	16	76	36.4	39	
	AAW97614	20	75	36.4	39	
Yeast ubiquitin	AAW46380	19	75	36.4	39	
Yeast ubiquitin	AAW01700	18	75	36.4	39	
Cholera toxin B/en	AAY87460	21	7	٠	39	
(TO	AAG02635	21	51	39.3	42	
Cholera toxin B	AAY87464	21	œ	•	43	
toxin	AAB74320	22	15		59	
Bovine rotavirus	AAB15526	21	15	•	61	
Cholera toxin B	AAB15525	21	15	•	61	
Cholera toxin B/en	AAY87461	21	12	•	62	
	AAR76748	16	23	71.0	76	
le	AAR85125	16	15	•	76	
CTP3 epitope o	AAP93498	10	15	71.0	76	

ALIGNMENTS

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RESULT 1
AAY87463
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                                                                                                                                                                                                                                                                          Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                          AAY87463 standard; peptide;
                                                                                                                  (UYBR-) UNIV BRISTOL.
                                                                                                                                            07-SEP-1998;
                                                                                                                                                                      07-SEP-1999;
                                                                                                                                                                                                                        WO200014114-A1
                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                              E. coli heat labile enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                   AAY87463;
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                             B-derived peptide,
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100.0 100.0 100.0 100.0 100.0 100.0 100.0 94.4 87.9 82.2 81.8 74.8

21 20 20 21 21 44 44

AAY87463 AAR72545 AAY41816 AAW95226 AAW95226 AAH66239 AAY87463 AAP50436 AAP50436 AAP50636

Heat labile toxin E coli verotoxin-1 Cholera toxin B/en Network polymer wh Network polymer of amino Sequence of amino Sequence of amino

WPI;

2000-256943/22.

Williams NA,

Hirst TR;

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

glycolipid receptor GM-1

E. coli heat labil ADP-ribosylating t Escherichia coli v E. coli heat-labil

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Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                   ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1;
Disclosure; Fig
                               other molecules
                                            New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes
                                                                                                                      Armstrong GD,
Oomen R, Read
                                                                                                                                                                                                                24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                           05-APR-1995
                                                                                                                                                                                                                                                                                                                          EP646599-A.
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                                                                                          WPI; 1995-132623/18.
                                                                                                                                                                                                                                                               23-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptide fragments of the Escherichia coli h labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR72545 standard; peptide; 93
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particularly preferred.
                                                                                                                                                                     (CONN-) CONNAUGHT LAB
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                                                                                                                       Cockle SA,
RJ, Stein
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94US-0251121.
                                                                                                                                                                                                                                                             94EP-0306219
<u>5</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin (verotoxin-1 B-subunit).
54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /or toxin-induced diarrhoea. Sequences AAY87460-Y87463
peptides of the invention, AAY87460 being
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Pred. No. 2.6e-11;
; Mismatches 0;
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RESULT 3
AAY41816
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CC involving analysis of the 3-dimensional form of the crystalline CC involving analysis of the 3-dimensional form of the crystalline CC holotoxin. The pertussis holotoxin modification process comprises: CC (1) identification of at least one amino acid (aa) residue of the CC crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline and function; (2) effecting mutagenesis (by removing or coperon; and (3) expressing mutant tox box in a Bordetella organism to pertussis holotoxin, by studying its 3-dimensional crystalline crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa)
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                      Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                       Example 3; Fig 5; 41pp;
                                                                                                                                                                                                                                                                                        New method for producing modified
                                                                                                                                                                                                                                                                                                                        WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
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Oomen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coli.
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                      RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       verotoxin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 107; DB 16;
Pred. No. 1.5e-10;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                     Loosmore
                                                                                                                                                                                                                                                                                        pertussis holotoxin
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                                                                                                                                                                                                                                                                                                                                                                     Klein MH,
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                                                                                                                                                                                                                                                                                                                                                                   Armstrong GD;
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The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying CC at least 1 site in a PT that interacts with a molecule that is capable of CC forming a complex with the holotoxin and which molecule is an effector cc molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of pT. The functional cc interacting site(s) are identified by analysing the three dimensional cc structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The three-dimensional structure coil binding and adjuvanticity of the PT. The present activity, mitogenicity.
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Best Local :
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an Alp-ribosylating toxin because the present of the present sequence of the present sequence represents and probability to the present toxin the present probability to the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modifications to e.g. enzymatic ac binding of pertussin holotoxin - b a molecule with crystalline toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1999
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RESULT 5
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Best Local
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                         pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other
                                                                     proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAX68340 to AAY68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                   Crystalline form of proteins which have
                                                 Sequence
                                                                                                                                                                                                                                  The present invention describes a
                                                                                                                                                                                                                                                            Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY68365 standard; Peptide; 93
                                                                                                                                                                                                                                                                                                                                                Hazes
                                                                                                                                                                                                                                                                                                                                                                                    (CONN-) CONNAUGHT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                         2000-136703/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                æ
            Similarity
                                                                                                                                                                                                                                                           Ψ
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                                                                                                                                                                                                                                                                                                                                                 0omen
                                                                                                                                                                                                                                                                                                                                                              Stein
                                                                                                                                                                                                                                                           Fig 5; 42pp; English.
                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0292968.
93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0467976
                                                                                                                                                                                                                                                                                   isolated pertussis hol functional resemblance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                             Cockle SA,
                                                                                                                                                                                                                                                                                                                                                                                                 LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107; DB 20;
Pred. No. 1.5e-10;
Mismatches 0;
            Score 107;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                              Loosmore
                                                                                                                                                                                                                                  crystalline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:26
                                                                                                                                                                                                                                                                                              holotoxin
1.5e-10;
thes 0;
                                                                                                                                                                                                                                                                                                                                                             Ś
                        DB 21;
                                                                                                                                                                                                                                  form of isolated
                                                                                                                                                                                                                                                                                                                                                              Klein MH,
                                                                                                                                                                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                               in studying
                        93;
                                                                                                                                                                                                                                                                                                                                                            Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Matches

0;

Mismatches

Indels

0;

Gaps

0;

Local

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21

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RESULT 6
AAB62339
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX Pert
KW Pert
KW 1ymp
XW 151e
OX Esch
XX 22-4
PR 21-y
PR 21-y
PR 31-y
PR 31-y
PR 31-y
PR 31-y
PR 31-y
PR 31-y
PR 51-y
PR 61-y
PR 6
RESULT 7
AAY87462
ID AAY8
XX
AC AAY8
XX
DT 03-J
                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin. Pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
  03-JUL-2000
                                              AAY87462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify of toxicity, cell binding or enzyme activity of PT and modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                AAY87462 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of toxicity, cel
identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 5; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hazes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6168928-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pertussis toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E coli verotoxin-1 B subunit SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB66239 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ymphocytosis-promoting factor;
                                                                                                                                                                                                                                35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is B,
                                                                                                                                                                                                                                                  GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-122260/13
                                                                                                                                                                                                                             GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                           Similarity 100
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cockle SA,
Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 93 AA;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0292968.
93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystal
                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structure; whooping cough; biological activity;
factor; histamine-sensitising factor;
                                                                                                                                                                                                                             55
                                                                                                   21
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                           Score 107; DB 22; Pred. No. 1.5e-10; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein MH,
                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Armstrong
                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GD;
                                                                                                                                                                                                                                                                                                                              0;
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RESULT 8
AAP50439
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                                                                                                                                                                                                                           ρy
                                                                                                                                                                                                                                                                                                                                                                                 CC toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC (SM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain CC for some of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the cha-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as cormal EtxB and CtxB subunits, except that they do not bind or cross link CC mormal EtxB and CtxB subunits, except that they do not bind or cross link CC They may also be used in medicine as an inhibitor for toxin-induced diarrhoea.

CT treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AX87460-Y87463
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1 - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-4-alpha-2 loop; GM-1
adjuvant; immune disorder;
Network polymer which comprises a series of composite labile toxin (LT)/heat-stable toxin (ST) polypeptide r
                                                01-JAN-1980
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                       represent preferred peptides of the invention, particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                               AAP50439
                                                                                                               AAP50439 standard; protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to peptide fragments of the Escherichia labile enterotoxin (Etx) and its closely related homologue, cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B/enterotoxin B-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                               _
                                                                                                                                                                                                              1 GETFQVEVPGSQHIDSQKKAI 21.
                                                                                                                                                                                             GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                           20; Conser
                                                                                                                                                                                                                                                                                                                          21
                                              (first entry)
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hirst TR;
                                                                                                                                                                                                                                                                                                                          AΑ;
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                                                                                                                                                                                                                                                                            94.48;
95.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62pp; English.
                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                            Score 101; DB 21;
Pred. No. 2.7e-10;
                                                                                                               A
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide,
                                                                                                                                                                                                                                                                                                                                                        n. Sequences AAY87460-Y87463
AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                             Indels
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 e E. coli heat-
repeating untis.
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                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholera
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     interpolypeptide cystine bonds formed between oxidized Cys residu of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
New synthetic polypeptide(s) for part of E.
                                                                                                                                                  WO8502611-A
                                                                                                                                                                        Synthetic
                                                                                                                                                                                            Heat-labile
                                                                                                                                                                                                                                                  01-JAN-1980
                                                                                                                                                                                                                                                                                           AAP50436 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic polypeptide(s) for part of E. coli enterotoxin useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W08502611-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-labile
                     WPI; 1985-159230/26
                                          Houghten
                                                                                     12-DEC-1983;
                                                                                                                                                                                                                                                                       AAP50436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghten RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1984;
                                                               (SCRI-) SCRIPPS CLINIC RES
                                                                                                        12-DEC-1984;
                                                                                                                              20-JUN-1985
                                                                                                                                                                                                               Network polymer which comprises a series of composite E. coli heat-
labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The repeating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCRI-) SCRIPPS CLINIC RES
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                    GETFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                 GETFQVEVPGSQHIDSQK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         units are bonded together by intramolecular ide cystine bonds formed between oxidized Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                     83US-0559469
                                                                                                        84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83US-0559469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84WO-US02030
                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               87.98;
                                                                                                                                                                                             heat-stable
                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB Pred. No. 9.5 0; Mismatches
                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                            toxin;
                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Lo
9.5e-09;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli enterotoxin(s
                                                                                                                                                                                            vaccine;
 coli enterotoxin(s
                                                                                                                                                                                                                                                                                                                                                                                                            Length 41
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RRESULT 10
AAP30600
ID AAP30
XX AAP30
XX AAP30
XX 21-AP
XX Chole
XX Clair
XX AP30
XX Chole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP3)264, AAP3)265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous contractions are applied.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The
                                                  a vaccine
                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The repeating units are bonded together by intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                        routes. For vaccines, pref. peptides having 15-30 AAs are without carriers. Unit dose when used as a medicament is 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1983-834645/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guyongruaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP95426-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP30600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP30600 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GXTFQVEVPGSQHIDSQK
                                                                                                                                                                                                                                                                                                                                   8; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Page 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                1-10mg of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arg at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raulais D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENT NAT RECH SCI
PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82FR-0009167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delmas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83EP-0401052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; E.coli infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids 350-75 of the cholera toxin B1 subunit which posns. 35, 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                     active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.2%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 88; DB Pred. No. 1.2e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siffert O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 46
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                                                                          50-500mg
                                                                                                     injected
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Sequence

47

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RESULT 12
AAP93498
ID AAP93
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AC AAP93
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AAP30265
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                                                                                                                   Query Match
Best Local S
Matches 16
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Best Local
                                                                                                                                                                                          The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
 AAP93498;
                                                                                                                                                                                                                                                                                                                         Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of amino acids 50-75 of the cholera carries an Arg at posns. 67 and 73.
                     AAP93498 standard;
                                                                                                                                                                                   a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                      Claim 7; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                           Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholera vaccine; therapy; E.coli infection;
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                       Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1983
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                                                                                     VEVPGSQHIDSQKKAI
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                                                                                                                     L Similarity
16; Conserv
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                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                           Raulais D,
A, Delmas
                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           CENT NAT RECH SCI
PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                              74.8%;
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Pred. No. 1.4e-07;
                                                                                                                              Score 80;
Pred. No.
                     3
                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      Siffert
                                                                                                               DB 4; L., 1.4e-06; 0;
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                                                                                                                                       Length 26
                                                                                                                                                                                                                                                                                                                                                                                                      Dodin
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                                                                                                                     Indels
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                                                                                                                    Gaps
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RESULT 13
AAR85125
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 epitope, of antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 198
N-PSDB;
                  03-MAY-1994;
                                                                                              Vibrio cholerae
                                                                                                                                                               Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                                                                                                             This sequence corresponds to the CTP3 epitope of the Cholera toxin subunit. The DNA sequence encoding this ligates to othersynthetic oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTP3 epitope of Cholera vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTP3
                                     02-MAY-1995;
                                                        09-NOV-1995
                                                                           WO9529701-A1
                                                                                                                                                                                                                        AAR85125
                                                                                                                                                                                                                                                                                                                                                                     therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant flagellin gene including sequence - for hetepitope, and expressed fusion proteins, useful in vaccines
                                                                                                                         Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen;
                                                                                                                                                                                 13-JUN-1996 (first entry)
                                                                                                                                                                                                      AAR85125;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marjarian WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-1990
                                                                                                                 intestines;
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO8910967-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STRD )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 itope, and emand antibodies.
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                                                                                                                                                                                                                                                                       VEVPGSQHIDSQKKA
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DB; AAN92414.
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                                                                                                                                                                                                                                                                                                             . Similarity 100. 15; Conservative
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                                                                                                                                                                                                                        standard;
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                                                                                                                 antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                              fig.4B; 137pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Cholera toxin B subunit; flagellin fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                    ΑA;
                 94IL-0109519.
                                     95WO-EP01661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stocker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88US-0190570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89WO-US01932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Cholera
                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                       71.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAD,
                                                                                                                 secretory; IgA
                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin B subunit
                                                                                                                                                                                                                                                                                                                      Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newton
                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMC;
                                                                                                                                                                                                                                                                                                             DB 10; 1
3.4e-06;
hes 0;
                                                                                                                                                                                                                                                                                                                               Length 15
                                                                                                                                                                                                                                                                                                              Indels
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
Chimeric
   WPI; 1995-275442/36
                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR76748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR76748 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aldehyde silica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent choleral pound to micro:particulate inert carrier, e.g. modified covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marks
                                      Hasty DL,
                                                                                                                  27-JAN-1994;
                                                                                                                                                     27-JAN-1995;
                                                                                                                                                                                         03-AUG-1995
                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                          (GXBI-) GX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue;
FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 25; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgA class.
                                      Klemm P,
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                                                                           BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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                                                                                                                                                     95WO-DK00042
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20..22
                                                                                                                                                                                                                                                                                                                                                            /note= "Linker peptide"
5..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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                                                                                                                                                                                                                                                                   "Represents FimH residue 226"
                                                                                                                                                                                                                                                                                                    "Linker peptide"
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Pred. No.
                                        Pallesen
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                                                                                                                                                                                                                                                                                                                                         toxin B
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3.4e-06;
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Best Local :
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                                                                                                                                  WPI;
                   Disclosure; Page 15; 62pp; English
                                                        glycolipid
                                                                                                                                                                                                                                                                                                                       16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY87461;
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                                                                                             Derivatives of Escherichia coli heat labile enterotoxins useful
                                                                                                                                                                                                          (UYBR-)
                                                        immunomodulators and for
jlycolipid receptor GM-1
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shows the inclusion of the B subunit into the FinH protein at position of the hepatitis B virus surface antigen pre-52 region into a different position of the rimH adhesin of type I fimbriae. Restiction site handles (BglII-sites) were introduced into the finH gene, and the foreign epitopes are then inserted in-frame. In the selected positions the insertion of the epitopes did not significantly alter the adhesive function of the FinH protein. The expression of the chimeric proteins on the surface of fimbriae on bacterial hosts illustrated the possibility of using bacterial adhesins as general presenters of foreign antigens and epitopes. These chimeric genes may be used in the production of variant finH adhesins which may be useful for targetting active compounds and microbial cells to locations comprising selected receptors to which the adhesins bind.
                                                                                                                                                                                                                                                           Vibrio cholerae.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                     Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a fragment of the the plasmid pLPA93 which was used in the production of fimH fusion genes comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                  Williams NA,
                                                                                                          07-SEP-1998;
                                                                                                                                               07-SEP-1999;
                                                                                                                                                                                                                        WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                                                           Cholera toxin B/enterotoxin B-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY87461 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the cholera toxin B subunit inserted into the fimH gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VEVPGSQHIDSQKKA 20
2000-256943/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
15; Conserv
                                                                         UNIV
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                                                                                                                                                                                                                                                                                                                   immune
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                                                                         BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                    Hirst TR;
                                                                                                            98GB-0019484
                                                                                                                                               99WO-GB02970
                                                                                                                                                                                                                                                                                                                   disorder;
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                                                                                                                                                                                                                                                                                                                   GM-1 ganglioside order; diarrhoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           peptide,
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5.7e-06
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                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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imH gene. This i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 23
                                                                                                                                                                                                                                                                                                                                       immunomodulation;
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                                                                                                                                                                                                                                                                                                                                                      В;
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CC The invention relates to peptide fragments of the Escherichia coli heat Clabile enterotoxin (Etx) and its closely related homologue, cholera CC toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the fefects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC Therefore, the peptides may be used in the production of a composition CC immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 CC represent preferred peptides of the invention, AAY87460 being CC particularly preferred particularly preferred.

Sequence 12 AA;

Query Match 57.9%; Score 62; DB Best Local Similarity 100.0%; Pred. No. 0.000 Matches 12; Conservative 0; Mismatches DB 21; I 0.00065; thes 0; Length 12; Indels 0; Gaps 0

밁 6 VEVPGSQHIDSQ 17 |||||||||||| 1 VEVPGSQHIDSQ 12

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Search completed: October 24, 2002, 15:35:04 Job time: 32.7049 secs

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/packfiles1.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-340-154-94
PCT-US95-09338-94
PCT-US95-09339-94
US-09-045-632-83
US-09-100-804-23
US-09-045-632-61
US-09-045-632-61
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US-08-467-974-26
US-08-467-976-26
US-08-67-976-26
US-08-90-082-514-26
US-08-709-173-35
US-08-709-177-35
US-08-709-177-35
US-08-833-678A-3
US-08-833-678A-3
US-08-232-815-2
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(without alignments)
42.570 Million cell updates/sec
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83, Appl
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US-08-292-968-26
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Sequence 53, Ap	US-09-218-950-53	4	76	29.0	31	ິດ
Sequence 53, Appl	US-08-284-391B-53	N	76	29.0	31	4
Sequence 29, Appl	US-08-332-562A-29	N	75	29.0	31	w
Sequence 10, Appl	US-08-849-480A-10	N	66	29.0	31	N
Sequence 6, Appli	US-08-255-558B-6	Н	28	29.0	31	Р
Sequence 14, Appl	US-08-693-696-14	ω	21		31	0
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Sequence 14, Appl	US-08-355-888A-14	_	21		31	œ
Sequence 16, Ap	US-08-418-893D-16	_	35		31.5	7
Sequence 1, Appli	US-09-100-802-1	4	76	29.9	32	0
Sequence 8, Appli	US-08-817-787-8	4	76		32	Çī
Sequence 1, Appli	US-08-817-787-1	4	76		32	4
Sequence 8, Appl:	US-09-357-746-8	w	76		32	ω
Sequence 8, Appli	060-8	N	76		32	N
Patent No. 5208144		0	41		32	_
Sequence 10, Appl	US-08-817-787-10	4	37		32	0
Sequence 3, Appli	US-08-817-787-3	4	37		32	9
Sequence 8, Appli	US-08-308-818-8	N	21	30.4	32.5	ω

ALIGNMENTS

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(*1b) 595-11
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY.
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Patent No. 5856122
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MEDIUM TYPE: Floppy
                                                                                                                                                     REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: KRISTRONG, Glen D
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Univ
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                      6) 595-1155
595-1163
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TOPOLOGY:
US-08-467-974-26
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US-08-467-974-26
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                                             Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                            TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                         REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/467,536
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                          FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Toronto
STATE: Ontario
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                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            LENGTH:
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GETFQVEVPGSQHIDSQKKAI 21
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                                            Similarity
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M5G 1R7
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                                                                                                                                                        93 amino acids
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Suite 701, 330 University Avenue
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KLEIN, Michel H.
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                                                                                                                linear
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                            100.0%; Score 107; DB 2; 100.0%; Pred. No. 2.7e-11; tive 0; Mismatches 0;
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RESULT 4
US-08-467-976-26
; Sequence 26, Application US/08467976
; Patent No. 6018022
; GENERAL INFORMATION:
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TOPOLOGY:
US-08-467-536-26
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                                                                                                                                                                             Matches
                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/110,947 FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/251,121 FILING DATE: 31-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                              35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                       LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/467,536 FILING DATE: 06-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
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                                                                                                                                                                           Local Similarity 100. es 21; Conservative
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                                                                                                                                  1 GETFQVEVPGSQHIDSQKKAI 21
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M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08467536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEIN, Penelope E COCKLE, Stephen A OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLEIN, Michel H. ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sim & McBurney ite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                      (416)
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                                                                                                                                                                                                                                                                                                                                                       595-1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bart
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                                                                                                                                                                                                                                                                                                                                                                                                    1038-455 MIS:vg
                                                                                                                                                                           Score 107; DB 2;
Pred. No. 2.7e-11;
; Mismatches 0;
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                                                                                                                                                Patent No. 6168928
GENERAL INFORMATION:
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/292,968
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/251,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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              APPLICANT: ARMSTRO
APPLICANT: HAZES, 1
TITLE OF INVENTION:
                                                             APPLICANT: STEIN, Penelope E. APPLICANT: COCKLE, Stephen A. APPLICANT: OOMEN, Raymond P. APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08 FILING DATE: 31-MAY-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08
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ADDRESSEE: Sim & McBurney
 NUMBER OF SEQUENCES:
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLASSIFICATION: 435
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ກາ 616892
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                               HAZES, Bart
                                               ARMSTRONG, Glen D.
                                                                                                                                   READ, Randy J.
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, Stephen A.
MODIFICATION OF PERTUSSIS TOXIN: 46
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US-08-350-884-35
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APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 2
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: U$/08/350,884
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
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LENGTH: 93 amino acids
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APPLICATION NUMBER: US/09/082,514
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 24-AUG-1994
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STREET: OTTY: Toronto
Ontaric
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CITY: Palo Alto
STATE: Californ:
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                                                                                    APPLICATION NUMBER: FILING DATE: 06-DEC
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STRANDEDNESS: si
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м5G 1R7
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                                                                                                                                                                                                                                                          California
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                                                                                                                                      Version
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
    Matches
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application Patent No. 5712145
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                                                                                                                                               INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                        REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/680,296 FILING DATE: 04-APR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     FILING DATE: 06-SEP-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: CHOO,
APPLICANT: KUO, (
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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  Local Similarity 42.9
nes 9; Conservative
                                                                                  LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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REGISTRATION NUMBER:
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Similarity 42.9%;
9; Conservation
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                                                                                                                                                                         (415) 494-0792
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                36.4%;
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 Score 39; DB Pred. No. 11; 3; Mismatches
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Pred. No.
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11;
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                                                                                                                                                                     Sequence 3, Application US/08833678A Patent No. 5989905
                        GENERAL INFORMATION:

APPLICANT: CHOO, QUI-LIM

APPLICANT: CHOO, QUI-LIM

APPLICANT: HAN, JANG

APPLICANT: HAN, JANG

APPLICANT: CHOE, JOONHO

TITLE OF INVENTION: HCV NS3 PROTEIN FRAGMENTS HAVING

TITLE OF INVENTION: HELICASE ACTIVITY AND IMPROVED SOLUBILITY

NUMBER OF ERQUENCES: 6
                                                                                                                                                                                                                                                                                                                                               Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/709,177 FILING DATE: 06-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
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CHIRON CORPORATION
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Pred. No.
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Intellectual Property - R440, P.O. Box 8097

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US-08-529-169A-3
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Patent No. 6194140
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,169A
FILLING DATE: 15-SEP-1995
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HCV NS3 PROTEIN FRAGMENTS HAVING TITLE OF INVENTION: HELICASE ACTIVITY AND IMPROVED SOLUBILITY NUMBER OF SEQUENCES: 6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIFICATION: 4325
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
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APPLICATION NUMBER: US 08
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
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CITY: Emeryville
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                             ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
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HAN, JANG
CHOE, JOONHO
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Patent No.
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                                                   Query Match
Best Local :
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Matches 9; Conserva
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                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: FAITELL!, Kevin M.
REGISTRATION UNMBER: 35,505
REFERENCE/DOCKET NUMBER: CIT-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207 363-0558
TELEFAX: 207 363-0528
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                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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LENGTH: 75 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3274
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TITLE OF INVENTION: SPLIT UBIQUITIN PROTEIN SENSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/232,815 FILING DATE: 22-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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1 GETFQVEVPGSQHIDSQKKAI 21
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                                      Conservative
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                                                                                                                          linear
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                                                   36.48;
42.98;
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42.9%;
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Pred. No.
                                                   Score 39;
Pred. No.
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                                                               Length 76;
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Patent No. 5714464
GENERAL INFORMATION:
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                                               SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 207 363-0558
TELEFAX: 207 363-0528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay
                                                                                                                                                                                                                                                                             APPLICANT: Piraino, Frank and Brandt, Curtis R TITLE OF INVENTION: Anti-Viral Mushroom Extraconumber of Sequences: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Johnsson, Nils
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: UBIQUITIN-BASED SPLIT PROTEIN SENSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TENGTH: 76 cm
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      COUNTRY: USA
ZIP: 53701-2113
                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/O FILING DATE: 07-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION: 514
              FILING DATE
                              APPLICATION NUMBER: US/08/468,274
                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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Pred. No.
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PCT-US95-04536-2
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GENERAL INFORMATION:
APPLICANT: California Institute of Technology
 Best Local Similarity Matches 9; Conserv
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                            TELEFAX: 207 363-0528 INFORMATION FOR SEQ ID NO:
                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 207 363-0558
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,906
FILING DATE: 07-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
ORGANISM: ROZ
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                              MOLECULE TYPE: protein
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HYPOTHETICAL:
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LENGTH: 76 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: UBIQUITIN-BASED SPLIT PROTEIN SENSOR
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                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                     NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US95/04536
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                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                              76 amino acids
36.4%;
ilarity 42.9%;
Conservative
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42.9%;
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Pred. No.
Score 39; DB 5;
Pred. No. 11;
3; Mismatches
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                            Length 76;
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RESULT 15
US-08-450-834-6
; Sequence 6, Application US/08450834
; Patent No. 5773705
; Patent No. 5773701
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; MOLECULE TYPE:
US-08-450-834-6
                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,709
FILING DATE: 31-DEC-1992
ATTORNEY/ACENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.92425
TELECOMMUNICATION: TELEPHONE: 608-251-500
TELEPHONE: 608-251-9166
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
TOPOLOGY: linear
TOPOLOGY: linear
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Search completed: October 24, 2002, 15:38:24
Job time: 12.0492 secs
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ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILDLE
COMPUTER: IBM PC COMPAILDLE
OPERATING SESTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,834
FILING DATE: 25-MAY-1995
                                                                                                                                                            Query Match 35.5%;
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vierstra, Richard D
APPLICANT: Hondred, David
APPLICANT: Callis, Judy
TITLE OF INVENTION: Ubiquitin Fusion Protein System for
TITLE OF INVENTION: Protein Production in Plants
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: P.O. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. B
CITY: Madison
STATE: WI
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                                                                            GKTITLEVESSDTIDNVKAKI 30
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Pred. No. 17;
3; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 100
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                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 24, 2002, 15:35:09; Search time 139.77 Seconds (without alignments) 52.884 Million cell updates/sec
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Copyright (c) 1993 - 2002 Compugen Ltd.
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18	18	22	0 0	ر د	19	16	ω	26	16	21	21	19	16	22	Н	20	20	19	19	16	16	26	22	22	81			14	21	22	19	22	26	21	21	21	21	21
US-09-482-611B-94	US-09-482-611-94	-09-857-841-	-09-620-1116-304	-00-630-111p	-09-516-277-	60-687	US-07-999-709-6	-409-	-796-	-09-708-4	-427-	-277-	-09-260-687-1	-761-	-us01-00663-3	-09-620-111B-304	-09-620-111B	-09-516	-09-516-277-	-09-260	-09-260-687-7	-60-177-646-3	884-456-3	US-09-884-455-35	483-799-	8-833-678-	7-680-296-35	-09-072-955A	-09-786-64	-008-60-	-09-595-	-09-866-066-	-60-188-162-4	-09-708-427-4	-09-708-427-4414	-09-758-463-76	-09-708-427-6	US-09-786-648-3
94,	Sequence 94, Appl	2,	٠.	٠ ک	0	e 6,	6, 7	e 18		Sequence 75825, A	3723	10,		Φ	37905,	3049,	3048	11,	7, 1	11,	7	3942, Ā	35,	35	ω.	ω	35, 2	27,	2, 7	11,	470,	e 35,	e 4		44143,	e 761, z	e 686	Sequence 3, Appli

ALIGNMENTS

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                                                                                                                     ; LOCATION: 45...65; OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable; OTHER INFORMATION: porcine E. coli US-09-786-648-5
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US-09-786-648-5
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09786648
GEMERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccinite Reference: 7438
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 5
                                        Matches
                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                    LENGTH: 21
TYPE: PRT
ORGANISM: E. coli
FEATURE:
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
1 GETFQVEVPGSQHIDSQKKAI 21
                                        Conservative
                                      100.0%; Score 107; DB 21; 100.0%; Pred. No. 1.4e-10; tive 0; Mismatches 0;
                                                                            Length 21;
                                        Indels
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                                      Gaps
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RESULT 3
US-08-110-947A-26
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US-08-110-947-10
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/110,947
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
REGISTRATION NUMBER: 28,946
REGISTRATION NUMBER: 28,946
                                                                                                                                                                                                                        Sequence 26, Application US/08110947A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08110947 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Surce
STREET: Davis Hwy.
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                APPLICANT: READ, Randy J
APPLICANT: STEIN, Penelope E
APPLICANT: COCKLE, Stephen A
APPLICANT: COCKLE, Stephen A
APPLICANT: KLEIN, Michel H
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OOMEN, Raymond I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                 1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
E: Shoemaker and Mattare, Ltd.
Suite 1203 Crystal Plaza I, 2001 Jefferson
Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker and Mattare, Ltd.
Suite 1203 Crystal Plaza I, 2001 Jefferson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEIN, Penelope E
COCKLE, Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Randy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 107; DB 5;
100.0%; Pred. No. 9.3e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038-303 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
               APPLICATION NUMBER: US/08/2
FILING DATE: 31-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TD NO:

ACTERISTICS:

3 amino acids

ATRANDEDNESS:

TOPOLOGY:

110-947
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,947A
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FAILOW Charles W
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                         STREET: Suite 70
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FALLOW, Charles W REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ch 100.0%; Score 107; DB 5; Similarity 100.0%; Pred. No. 9.3e-10; 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                        Sim & McBurney
BER: 24,973
NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MODIFICATION OF PERTUSSIS TOXIN
                                                                                               US 08/110,947
                                                                                                                                                                                                                                                                                                                                                                                                                                              46
                                                                                                                                                                        US/08/251,121
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   1038-335
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                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 93;
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COMPUTER:

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-786-648-4
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                                                                                                                                                                                                                                                                                     RESULT 6
US-08-732-371-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Williams, Neil Andrew
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine
TITLE OF INVENTION: Adjuvants
TITLE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
FENGTH: 21
                                                                                                                                                                                                                                                      Sequence 1, Application US/08732371 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09786648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                      APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: INFECTING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 21; Conserv
                                                    COUNTRY:
                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                       GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                        GETFQVEVPGSQHIDSQKKAI 21
                                    20004
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 95.: 20; Conservative
                                                                 D.C.
                                                                                                  419 Seventh Street, N.W., Suite 300
                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                        MIRELMAN, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                       94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 21;
pred. No. 1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 6; Pred. No. 9.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
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RESULT 7
US-08-732-371A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08732371A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: IL 109519 FILING DATE: 03-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                 REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                           FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Relicurrent APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VACCINES FOR ORAL TITLE OF INVENTION: INFECTING AGENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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MARKS, Robert S.
SELA, Michael
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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RESULT 9
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                                                                                                                                                                                                                                                                                              Sequence 6862, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 6862
LENGTH: 91
TYPE: PRT
           ORGANISM: Arabidopsis thaliana FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..91
OTHER INFORMATION: Xaa is any an NAME/KEY: misc_feature
LOCATION: 1..91
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Best Local
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                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                             TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                 FILE REFERENCE: 2750-1243P
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TYPE: PRT
ORGANISM: E.
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION: Ceres Seq. ID 1816431
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0.0027;
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; OTHER INFORMATION: Ceres Seq. US-09-708-427-44143
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Best Local S
Matches 11
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SEQ ID NO 761
LENGTH: 99
   Matches
               Query Match
Best Local
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APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44143,
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Best Local
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                                                                                                                                                                                                                                                           FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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ORGANISM: Homo:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/758,463
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
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                                                                                         LOCATION: 1..61
OTHER INFORMATION: Xaa is
NAME/KEY: misc_feature
LOCATION: 1..61
                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                   TYPE: PRT ORGANISM: Zea mays subsp.
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                   ENGTH: 61
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nes 11; Conserv
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8; Conserv
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               40.2%;
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Pred. No.
               Score 43; DB Pred. No. 36;
                                                                          ID 1848967
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31;
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19;
                            21; Length 61;
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RESULT 13
US-60-188-162-4087
US-60-188-162-4087
Sequence 4087, Applicat
GENERAL INFORMATION:
FAITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
                                                                              RESULT 14
US-09-866-066-35
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; LCCATION: 1..76
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-441142
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                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/188,162
CURRENT FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 5094
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4087
                                                                                                                                                                                        Query Match
Best Local Similarity 53...
Best Focal Similarity 53...
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                Sequence 35, Application US/09866066 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Benjamin, Christopher APPLICANT: Roberds, Steve APPLICANT: Ruble, Cara
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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LOCATION: 1..76
OTHER INFORMATION: Xaa is
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42 GSTSRTEVPGQSHHD 56
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Pred. No.
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; NAME/KEY: misc_feature
; LOCATION: (). ()
; OTHER INFORMATION: Xaa is any aa,
US-09-595-298A-470
                                                                      Db
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US-09-595-298A-470
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Search completed: October 24, Job time: 140.77 secs
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER PA
SOFTWARE: PA
; SEQ ID NO 470
"ENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00229, US1
CURRENT APPLICATION NUMBER: US/09/866,066
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/207,152
PRIOR APPLICATION NUMBER: 60/207,257
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,257
PRIOR APPLICATION NUMBER: 60/207,257
PRIOR APPLICATION NUMBER: 60/207,257
PRIOR APPLICATION NUMBER: 60/207,257
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LENGTH: 51
TYPE: PRT
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APPLICANT: ALEXANDROV, Nicko
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-0953P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 470, Application US/09595298A
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Best Local :
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CURRENT FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 2756
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 91
TYPE: PRT
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SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(91)
OTHER INFORMATION: Ceres
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                                                                                                                                   38.3%;
Local Similarity 35.3%;
les 6; Conservation
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Local Similarity 58.3%;
nes 7; Conservative
                                                                      37 QSLLVKVPGKQHVSEKE
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Result
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US-09-791-537-120702
US-09-791-537-140209
US-10-155-881-12211
US-10-219-999-59647
US-10-155-881-12211
US-10-182-995-28451
US-10-182-995-28451
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US-10-182-995-28451
US-10-182-995-28451
US-10-182-995-28451
US-10-182-997-26224
US-10-203-136-377905
US-10-203-137-37905
US-10-203-139-36373
US-09-513-996A-39502
US-09-513-996A-39502
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US-09-620-393B-3233
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38 35.5 72 5 US-09-791-537-11043 38 35.5 76 5 US-09-620-393B-536 38 35.5 76 5 US-09-791-537-81362 38 35.5 76 5 US-09-791-537-81362 38 35.5 76 5 US-09-791-537-81362 38 35.5 76 5 US-09-620-393B-521 38 35.5 77 5 US-09-620-393B-521 38 35.5 77 5 US-09-935-625-11032 38 35.5 77 5 US-09-935-625-11032 38 35.5 77 5 US-09-935-625-11895 38 35.5 77 5 US-09-935-625-11895 38 35.5 77 5 US-09-935-625-12721 38 35.5 77 5 US-09-935-625-12721 38 35.5 77 5 US-09-935-625-12721 38 35.5 77 5 US-09-935-625-128647 38 35.5 77 5 US-09-935-625-128647 38 35.5 77 5 US-09-935-625-21350	45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	33	32	31	30	29	28
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	103413,	103174,	27445, A	24220, A	21350, A	18895, A	18647, A	15721, A	11032, A	6721, Ap	2479, Ap	5214, Ap	870, App	34217, A	81362, A	81335, A	5363, Ap	110433,

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; Sequence 761, Application US/10217607
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION: NUCLeic Acids, Proteins, and
; FILE REFERENCE: PMO11C1N
; CURRENT APPLICATION NUMBER: US/10/217,607
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 09/758,463
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FITTLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1068p
CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: Patentin version 3.0
SEQ ID NO 3233
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Ceres Seq. ID 1385062 US-09-620-393B-3233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3233, Application US/096203931 GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..84
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1..84
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Pred. No. 8.
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RESULT 3
US-09-791-537-81337
Sequence 81337, Application US/09791537
GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (9)
OTHER IMPORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-217-607-761
                                                         ; ORGANISM: Neurospora crassa US-09-791-537-137751
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US-09-791-537-137751
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; ORGANISM: Dictyostelium discoideum
US-09-791-537-81337
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                                                                                        CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 137751
LENGTH: 76
TYPE: PRT
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       Sequence 137751, Application US/09791537 GENERAL INFORMATION:
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LENGTH: 76
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 761
                                                                                                                                                                                                              APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
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APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TILE REFERENCE: 261/210
CURRENT FILING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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TYPE: PRT
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
Tatches 9; Conserve
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; OTHER INFORMATION: X is an unknown amino acid US-09-791-537-151859
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US-10-219-999-51216
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PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 51216
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APPLICANT: Edgerton, Mi
APPLICANT: Hinkle, Greg
APPLICANT: KOValic, Dav
APPLICANT: Liu, Jingdon
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Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 151859
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TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
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TYPE: PRT
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Local Similarity 42.9%;
hes 9; Conservative
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5 TLSVQVFGGNHLVEFKKAI 23
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Kovalic, David K.
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                                                                  Conservative
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Pred. No. 40;
4; Mismatches
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FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 15305
SOOTWARR: Patentin version 3.0
SEQ ID NO 120704
LENGTH: 62
TYPE: PRT
ORGANISM: Phreatamoeba balamuthi
US-09-791-537-120704
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Best Local Similarity
Thes 9; Conserve
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US-09-791-537-120702
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 120702
LENGTH: 62
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GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
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Best Local S
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property -
                                                      NUMBER OF SEQUENCES:
                                                                                        TITLE OF
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9; Conserv
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                                                                    INVENTION: HCV NS3 PROTEIN FRAGMENTS HAVING HELICASE ACTIVITY AND IMPROVED S
                                                                                                      CHOO, QUI-LIM
HAN, JANG
CHOE, JOONHO
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Pred. No.
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Pred. No.
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   R440, P.O. Box 8097
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RESULT 10
US-09-791-537-81370
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Best Local Similarity 42...
Conservative
                                                                                                                                                           SEQ ID NO 81370
LENGTH: 76
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 81370,
                                   Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SED ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                       APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek APPLICANT: Danzer, Josep
                                                                                                                                                                                                                                                                   APPLICANT: DATZET, JOSEPH TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: n/a
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GKTITLEVESSDTIDNVKSKI 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/483,799
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/529,169
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,643
FILING DATE: 30-Aug-2002
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 0100.005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3274
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                Application US/09791537
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                                                     36.4%;
42.9%;
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                                                     Score 39; DB Pred. No. 74;
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                                     Mismatches
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                                                                    Length 76;
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                                     Indels
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10 GKTITLEVESSDTIDNVKSKI 30

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US-10-219-999-59647
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US-10-155-881-12211
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US-09-791-537-140209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-791-537-140209
                                                                             Sequence 59647, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwel
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 12211
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Best Local
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LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lutilya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-10(52726)C CURRENT APPLICATION NUMBER: US/10/219,999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dotson, Stanton APPLICANT: Kovalic, David
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT ENTICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
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                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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TYPE: PRT
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Local Similarity 33.38;
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5; Conservative
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Liu, Jingdor
                                                              Stein, Joshua
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RESULT 15
US-10-182-995-28451
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Best Local S
Matches S
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SEQ ID NO 74565
LENGTH: 48
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                         Sequence 28451, Application US/10182995 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
FILE REFERENCE: PB 0004 WO 1
CURRENT APPLICATION NUMBER: US/10/182,995
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Molecular Dynamics, APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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9; Conserv
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Hanzel, David K.
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                                                                                                                                                                                                                                                                           Chen, Wensheng
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   03 October
NUMBER: US 6
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r 2000 (03.10.00)
60/236,359
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Pred. No.
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63;
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PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 00/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)

SOFTWARE: MOLECULAR Dynamics Sequence Listing Engine
SEQ ID NO 28451
TYPE: PRT
ORGANISH: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL109658.5
FEATURE:
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
FEATURE:
OTHER INFORMATION: EST_HUMAN HIT: AV651727.1, EVALUE 4.00e-15
US-10-182-995-28451

Query Match
Best Local Similarity 46.2%; Pred. No. 68;
Best Local Similarity 46.2%; Pred. No. 68;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 EVPGSQHIDSQKK 19
Db 23 DLPGKSHLISKKX 35

Search completed: October 24, 2002, 15:47:34

Job time: 45.7869 secs
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 100
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PIR_71:*
1: pir1:*
2: pir2:*
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4: pir4:*
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107
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
32	32	32	32	32	32	32	32	32	32	32	32	32	32	ω	သ
		29.9													
79	78	77	76	76	76	76	76	76	75	74	51	38	35	95	82
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S77831	H71922	S34334	S42750	S28203	A26087	UQUYSF	ОВО	UHQU	A84102	UQFFM	AG2245	F60657	T02997	T14743	D84387
hypothetical prote	acyl carrier prote	ubiquitin - Leishm	polyubiquitin UB2	ubiquitin – rabbit	ubiquitin - fruit	ubiquitin - fall a	ubiquitin - bovine	ubiquitin - human	carbon storage reg	ubiquitin - Medite	hypothetical prote	circumsporozoite p	sigma-E factor reg	hypothetical prote	hypothetical prote

ALIGNMENTS

RESULT 2 C95152 IS66 family element, Orfl [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Apecies: O3-Aug-2001 #sequence_revision O3-Aug-2001 #text_change O3-Aug-2001 C;Accession: C95152 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris, A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Residues: 1-79 <kur></kur>	Query Match 43.0%; Score 46; DB 2; Length 91; Best Local Similarity 47.6%; Pred. No. 3.2; Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0; Qy 1 GETFQVEVPGSQHIDSQKKAI 21 Db. 58 GKTFNLEVKGSEIIQQVKNMI 78	RESULT 1 C96580 hypothetical protein F15I1.6 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96580 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallol ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719 A;Residues: 1-91 <sto> A;Coss-references: GB:AE005173; NID:g4587538; PIDN:AAD25769.1; GSPDB:GN00141 C;Gene: F1511.6 A;Map position: 1</sto>

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RESULT 3
H95167
IS66 family
                                                                                        C;Superfamily: acyl carrier protein; acyl carrier C;Keywords: carrier protein F;1-72/Domain: acyl carrier protein homology <ACP>
                                                                                                                                                                                                                                                     R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Wature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter A;Reference number: A81250; MUID:20150912

A;Accession: G81388
                                                                                                                                                                                                                                                                                                                                                                acyl carrier protein Cj0441 [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS66 family element, Orf1 [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C;Accession: H95167
20
                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-77 < PAR>
A; Cross references: GB: AL139075;
A; Experimental source: serotype (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005672; PIDN:AAK75412.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1314
                                                                                                                                            A; Gene: acpP; Cj0441
                                                                                                                                                            C; Genetics:
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A; Residues: 1-79 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Atthors: Loftus, B.J.; Yang, F.; Smith, H.O.; A; Title: Complete Genome Sequence of a virulent A; Reference number: A95000; MUID:21357209; PMID: A; Accession: H95167
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S.L.; Lewis,
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M.R.;
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Radune, D.; Holtzapple,
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Whitehead, S.;
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R; Belknap, W.
submitted to the EMBL Data
A; Reference number: S19798
A; Accession: S19799
A; Molecule type: mRNA
                                                                                 ubiquitin - potato
C;Species: Solanum tuberosum (potato)
C;Date: 30-Jun-1992 #sequence_revision
C;Accession: S19799; S19801; S19800
                                                                                                                                                                                                                                                                                                                                                                 A;Description: protein degradation C;Superfamily: ubiquitin; ubiquitin homology C;Keywords: nucleus; polyprotein; protein deg F;1-76/Product: ubiquitin #status predicted < F;1-76/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18, 6449, 1990
A;Title: A movel form of ubiquitin found in A;Title: A movel form S12114; MUID:91057153
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A; Residues: 1-76 <VIE>
C; Superfamily: ubiquitin; ubiquitin homology
C; Keywords: protein degradation
E; 1-76/Domain: ubiquitin homology <UBH>
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Biochemistry 25, 3105-3108, 1980
A; Title: Complete amino acid sec
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C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986
C;Accession: A02576
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A; Residues: 1-76 <FOS>
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A; Accession: A02576
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9; Conservative
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ubiquitin precursor - wheat (fragment)
C:Species: Triticum asstivum (common wheat)
C:Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
C:Accession: S16263
R;Joshi, C.P.; Weng, J.; Nguyen, H.T.
Plant Mol. Biol. 16, 907-908, 1991
A;Title: Wheat ubiquitin gene exhibits a conserved protein coding region and a A;Reference number: S16263; MUID:91316227
A;Accession: S16263
A;Molecule type: mRNA
A;Residues: 1-77 <JOS>
A;Cross-references: EMBL:X56601; NID:g21899; PIDN:CAA39938.1; PID:g21900
C;Reywords: polyprotein
F;1-76/Product: ubiquitin #status predicted <MAT>
F;1-76/Domain: ubiquitin homology <UBH>
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A;Cross-references: EMBL:Z11671; NID:g21603; PII
A;Accession: S19801
A;Molecule type: mRNA
A;Residues: 1-48 <BEL2>
A;Cross-references: EMBL:Z11672; NID:g21607; PII
A;Accession: S19800
A;Molecule type: mRNA
A;Residues: 37-77 <BEL3>
A;Cross-references: EMBL:Z11673; NID:g21605; PII
C;Superfamily: ubiquitin; ubiquitin homology
C;Keywords: protein degradation
F;1-76/Domain: ubiquitin homology <UBI>
                                                                                                                                            degenerate transposase (orf1) [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: B98034
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehe. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McY., P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jas A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98034
A;Status: preliminary
                                          A;Cross-references:
C;Genetics:
A;Gene: IS1381-trun
                                                                                                           A; Molecule type: DNA
A; Residues: 1-79 < KUR>
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9; Conserv
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                                                                                    GB:AE007317; PIDN:AAL00103.1; PID:g15458942;
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Pred. No.
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Pred. No.
Score 38;
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                                                                                    GSPDB:GN00174
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RESULT 12
$12161
$12161

polyubiquitin - large-leaved lupine (fragment)
C;Species: Lupinus polyphyllus (large-leaved lupine)
C;Date: 21-Nov-1993 #sequence_revision 17-Jul-1998 #
C;Accession: $12161
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-88 <FONS
A; Cross-references: EMBL: X13251
A; Cross-references: EMBL: X13251
C; Superfamily: ubiquitin; ubiquitin homology
C; Keywords: polyprotein; protein degradation
F; 12-11/Product: ubiquitin (fragment) *status
F; 12-87/Product: ubiquitin *status predicted
F; 12-87/Domain: ubiquitin homology <UBH>
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A;Gene:
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87520
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fortin, M.G.; Purohit, S.K.; Verma, D.P.S.
Nuccleic Acids Res. 16, 11377, 1988
A;Title: The primary structure of soybean (G
A;Reference number: S02222; MUID:89083578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin precursor - soybean (fragment)
N;Alternate names: polyubiquitin
C;Species: Glycine max (soybean)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Aug-1996
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A; Residues: 1-80 <STO>
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9; Conser
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A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AG3217
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R;Wood, D.W.; Setubal, J.C.; Kaul, R;Wood, D.W.; Setubal, J.C.; Kaul, erage, G.; Gillet, W.; Grant, C.; (Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                    RESULT 14
AG3217
hypothetical protein Atu5470 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S62680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Keywords: nucleus; polyprotein; protein degradation F;1-22/Product: ubiquitin (fragment) #status predicted F;1-22/Domain: ubiquitin homology (fragment) <UBH1>F;23-98/Product: ubiquitin #status predicted <UBH2>F;23-98/Domain: ubiquitin homology <UBH2>
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 A; Experimental
                   A; Cross - references:
                                   A: Residues:
                                                   A; Molecule type:
                                                                     A;Status: preliminary
                                                                                                                                       ster, E.W.
                                                                                                                                                       A; Authors: Yoo,
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A; Residues: 1-99 < RED>
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R; Redkar, R.J.; Lemke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquitin/ribosomal protein S27a fusion protein - Em
C;Species: Emericella nidulans, Aspergillus nidulans
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Nucleic Acids Res. 18, 6424
A;Title: Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence
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A; Cross-references: EM
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9; Conserv
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 source:
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 GB:AE008687; |
De: strain C58
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                                                                                                                                                       Y.; Biddle,
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homology <UBH>
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          PIDN: AAL46157.1;
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Guenthner, I
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                PID:g17743927;
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Search completed: (Job time : 15.8361

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F;3-74/Domain: acr-
F;38/Binding site:
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 i
C;Accession: S77465; S13820; S56069
C;Accession: S77465; S,; Kotani, H.; Tanaka, A.; Asar
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asar
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada,
DNA Res. 3, 109-136, 1996
В
                                  οy
                                                                                                                                                  C;Superfamily: acyl carrier protein; acyl carrier protein homology C;Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; F;3-74/Domain: acyl carrier protein homology <ACP> F;3-74/Domain: acyl carrier protein homology <ACP> C;KeyBinding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                            A;Description: carrier of the growing fatty acid A;Pathway: fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1, 'D', 3-20; 4! A; Accession: $56069
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A;Title: Purification and characterization
A;Reference number: S13819; MUID:91065389
A;Accession: S13820
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A;Gene: Atu5470
A;Genome: plasmi
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A; Residues: 1-77 <KAN>
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N;Alternate names: protein sll1068
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A; Residues: 21-22, 'G', 24-45
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STRAIN=ST. LAWRENCE 74 / SL 74 /
MEDLINE=91323720; PubMed=1650731;
                                                                                                                  Taccioli G.E., Grotewold E., Alsemberg G.O., "Ubiquitin expression in Neurospora crassa: a polyubiquitin gene.";
Nucleic Acids Res. 17:6153-6165(1989).
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STRAIN-ST. LAWRENCE 74 / SL 74 /
MEDLINE-89386647; PubMed-2549509;
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InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
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                                                         (UBII OR RPL40A OR YIL1148W) AND (UBI2 OR RPL40B OR YIL1167W OR L9470.14) AND (UBI4 OR Saccharomyces cerevisiae (Baker's yeast), Candida albicans (Yeast), and Cryptococcus neoformans (Filobasidiella neoformans) Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Carcharomycetales; Saccharomycetales; 
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EMBL; U01220; AAA56880.1; ALT_TERM.
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MEDLINE=85061630; PubMed=6095120;

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MEDLINE-94205265; PubMed-8154186;
Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.(
Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J
"The complete sequence of a 15,820 bp segment of Saccharomyces
cerevisiae chromosome XI contains the UBI2 and MPL1 genes and t
new open reading frames.";
Yeast 9:1349-1354(1993).
                                                                                                                                                                                                            [8]
SEQUENCE FROM N.A.
SPECIES=C.neoforma
                                                                                                                                                                                                                                                                                                                  SPECIES=C.albicans;
Bailey D.A., Gow N.A.R.,
Submitted (SEP-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S.cerevisiae; STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87275838; PubMed-3038523;
Oezkaynak E., Finley D., Solomon M.J., Varshavsky A.;
"The yeast ubiquitin genes: a family of natural gene fusions.";
EMBO J. 6:1429-1439(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oezkaynak E., Finley D., Varshavsky A.;
"The yeast ubiquitin gene: head-to-tail repeats encoding polyubiquitin precursor protein.";
Nature 312:663-666(1984).
                                                                     SPECIES=S.cerevisiae;
MEDLINE=95340540; PubMed=7615550;
Johnson E.S., Ma P.C.M., Ota M., Varshavsky A.;
"A proteolytic pathway that recognizes ubiquitin as
                                                                                                                                                                     MEDLINE=95369720; PubMed=7642124;
Spitzer E.D., Spitzer S.G.;
"Structure of the ubiquitin-encoding genes of Cryptococcus neoformans.";
SPECIES=S.cerevisiae;
MEDLINE=95166210; PubMed=7862120;
                                                             "A proteolytic signal.";
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SPECIES=C.albicans;
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MEDLINE=94205265; Pub
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                      MUTAGENESIS OF LYSINE RESIDUES
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                                                                                                                                                    Gene 161:113-117(1995)
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                                                  Biol.
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                                                  Chem.
                                                                                                                                                                                                                 neoformans; STRAIN=ATCC 6352;
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                                                 270:17442-17456(1995)
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; STRAIN=ATCC 26555;
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or send a
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"A ubiquitin mutant with specific defects in DNA repair and multiubiquitination.";

Mol. Cell. Biol. 15:1265-1273(1995).

Mol. Cell. Biol. 15:1265-1273(1995).

-i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOM BIOGENESIS AND DNA REPAIR.

-i- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-i- MISCELLANEOUS: UBII AND UBI2 ARE SYNTHESIZED AS A POLYPROTEIN WORL COPY OF UBIQUITIN FUSED TO RIBOSOMAL PROTEIN S37. UBI3 IS A POLYPROTEIN WITH ONE COPY OF UBIQUITIN FUSED TO ANOTHER RIBOSOM
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                                                                       modified and this statement is not removed
                                                                                                                                                                               between
                                                                                                                                                                                                                This
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                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                     EXACT HEAD TO TAIL REPEATS OF UBIQUITIN, THERE IS A FINAL AMINO-ACID (ASN) AFTER THE LAST REPEAT.
MISCELLANBOUS: IN C.ALBICANS UB14 IS A POLYPROTEIN CONTAINING EXACT HEAD TO TAIL REPEATS OF UBLQUITIN, THERE IS A FINAL AMINO-ACID (PHE) AFTER THE LAST REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN.
MISCELLANEOUS: IN S.CEREVISIAE UBI4 IS A POLYPROTEIN CONTAINING
s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                        non-profit
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institutions as long as its content
                                (See http://www.isb-sib.ch/announce/
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HSSP; P02248; 1UBI. SWISS-2DPAGE; P04838; YEAST. SGD; S0001410; RPL40A. SGD; S0001802; RPL40B. SGD; S0004157; RPS31. SGD; S0004157; UBI4. BINDING PRINTS; SITE SITE Nuclear protein; InterPro; IPR000626; Ubiquitin. Pfam; PF00240; ubiquitin; 1. PRINTS; PR00348; UBIQUITIN. EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2; EMBL; MUTAGEN MUTAGEN EMBL; R; A22696; UQBY.
R; C29456; UQBYR7.
R; A29456; A29456.
R; B29456; B29456.
R; D29456; D29456. ; Z28319; CAA82173.; ; U17246; AAB67466.; ; Z54197; CAA90901.; ; Z38059; CAA86130.; Z38059; CAA86130 U32627; AAA84868 U16992; AAA82979 X05730; CAA29197.1; X05731; CAA29198.1; X73541; CAA51949.1; X05729; CAA29196.1; X01473; SM00213; 63 48 76 29 48 CAA25704.1; CAA25706.1; CAA29195.1; UBQ; Polyprotein; 48 76 29 63 48 ALT_TERM.
ALT_TERM. UBIQUITIN ADDUCTS.

CONJUGATION TO ACCEPTOR P
K->R: DEFICIENCY IN UBIQU
CONJUGATE FORMATION.
K->R: DEFICIENCY IN UBIQU CONJUGATE FUNCTION. K->R: DEFICIENCY CONJUGATE FORMATION UBIQUITIN ADDUCTS.
INVOLVED IN UB-UB LINKAGES UBIQUITIN ADDUCTS.
INVOLVED IN UB-UB LINKAGES Multigene family; DNA repair.
INVOLVED IN UB-UB LINKAGES OF UBIQUITIN-PROTEIN UBIQUITIN-PROTEIN TOR PROTEINS.
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RESULT 4

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ID UGIO_CO

ID UGIO_CO

ID UGIO_CO

ID O1-FEB

DT 01-FEB

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P19848;
01-FEB-1991 (Rel. 1
01-FEB-1991 (Rel. 1
15-DEC-1998 (Rel. 3
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SEQUENCE
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PIR; S1:
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Nucleic Acids Res. 18:6449-6449(1990).

Nucleic Acids Res. 18:6449-6449(1990).

-i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91057153; PubMed=2173831;
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48 NECESSARY FOR BRAN
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   23-OCT-1986
23-OCT-1986
15-DEC-1998
Ubiquitin.
MEDIINE-90324239; pubMed-2165066; Callis J., Raasch J.A., Vierstra R.D.; Tubiquitin extension proteins of Arabilocalization, and expression of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica rapa (Turnip).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine

NCBI_TaxID=3847, 3888, 4498, 4499, 4513, 4565, 4577, 4232, 3702, 3

3874, 4081, 4113, 4006, 4096, 4686, 4530, 4043, 51350;
                                                                                                                         Burke T.J., Callis J., Vierstra R.D.; "Characterization of a polyubiquitin Mol. Gen. Genet. 213:435-443(1988).
                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of a full length cDNA clone encoding polyubiquitin gene from Pisum sativum."; Nucleic Acids Res. 17:10100-10100(1989).
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Nicotiana sylvestris (Wood tobacco),
Asparagus officinalis (Garden asparagus),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean),
Pisum sativum (Garden
Avena sativa (Oat),
Avena fatua,
                                                                       SEQUENCE FROM N.A. (UBQ1; UBQ2; SPECIES-A.thaliana; STRAIN-CV. (
                                                                                                                                                                              SPECIES-A.thaliana; STRAIN-CV. CO
MEDLINE-89039731; PubMed-2460733;
                                                                                                                                                                                                                                                     Avena sativa.
Biochemistry
                                                                                                                                                                                                                                                                                       "Complete amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-P.sativum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fortin M.G., Purohit S.K., Verma D.P.S.;
"The primary structure of soybean (Glycine identical to other plant ubiquitins";
Nucleic Acids Res. 16:11377-11377(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress),
Lupinus albus (White lupine),
Lupinus polyphyllus (Large-leaved lupine),
Lycopersicon esculentum (Tomato),
                                                                                                                                                                                                                 SEQUENCE FROM N.A. (UBQ4)
                                                                                                                                                                                                                                                                                                         Vierstra R.D., Langan
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house R.N., Wata
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tobacco."; J. Biol. Chem.

265:12486-12493(1990)

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"Sequence analysis and transcriptional regulation polyubiquitin transcripts from maize."; nrant mol. Blol. 12:619-632(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=T.aestivum; STRAIN=CV. MUSTANG; TIS

MEDLINE=91316227; PubMed=1650258;

Joshi C.P., Weng J., Nguyen H.T.;

"Wheat ubiquitin gene exhibits a conserved

a diverged 3' non-coding region.";
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"Two ubiquitin-long-tail fusion
direct repeats in barley.";
Gene 94:165-171(1990).
                                                                                                                                                                                                                                                                          SPECIES=L, Polyphyllus;
MEDLINE=91057134; PubMed=2173830;
Perrey R., Warskulat U., Wink M.;
"Molecular cloning of a cDNA for the ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gausing K., Barkardottir R.;
"Structure and expression of ubiquitin
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                     extension protein-encoding Gene 139:201-205(1994).
                                                                                                                                                                                                                                   polyphyllus
Nucleic Acid
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                                                                                       Jacinto A., Neves A.M., Rodrigues-Pousada C.;
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                                      "Cloning and characterization of two ubiquitin::79-amino-acid extension protein-encoding fusion genes from Lupinus albus.";
                                                                                                                                       MEDLINE=94156199; PubMed=8112604;
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107:205-212(1991).
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SPECIES-S.tuberosum; STRAIN-CV. LEMHI RUSSET; TISSUE-TI
MEDLINE-94154225; PubMed-8111011;

Garbarino J.E., Belknap W.R.;

"Isolation of a ubiquitin-ribosomal protein gene (ubi3 and expression of its promoter in transgenic plants.";

Plant Mol. Biol. 24:119-127(1994).
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SPECIES-L.esculentum; TISSUE-Root;
SPECIES-L.esculentum; TISSUE-Root;
MEDLINE-92032784; PubMed-1557246;
Hoffman N.E., Ko K., Milkowski D., Pichers
"Isolation and characterization of tomato
encoding the ubiquitin gene ubi3.";
Plant Mol. Biol. 17:1189-1201(1991).
Acanthamoeba castellanii (Amoeba) Eukaryota; Acanthamoebidae; Acant NCBI_TaxID=5755;
                                                                                                                                                                                                                                           SPECIES=O.sativa;
MEDLINE=93271454;
Nishi P., Hashimo
                                                                                                                                                                                                                                                                                         Davies K.M., King G.A.;
Davies K.M., King G.A.;
"Isolation and characterization of Asparagus officinalis L.
clones encoding two forms of ubiquitin mRNA.";
clones encoding two forms of 21:153-159(1993).
                                                                                                                                                                                                                                                                                                                                                                                            "Ubiquitin genes are differentially cultures of Nicotiana sylvestris and stresses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-N.sylvestris; TISSUE=Leaf; MEDLINE=93099242; PubMed=1281439; Genschik P., Parmentier Y., Durr A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91216447; PubMed-1850710; Agarwal M.L., Cullis C.A.; "The ubiquitin-encoding multigene usitatissimum.";
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Matches 8
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P22589;
01-AUG-1991
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                                                                                               ubiquitin.";

Plant Mol. Biol. 17:799-811(1991).

-I- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                MEDLINE-92003691; PubMed-1655113; Pieterse C.M.J., Risseeuw E.P., Davidse L.( "An in planta induced gene of Phytophthora
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ISOLATE 88069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
SEQUENCE
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between
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Phytophthora infestans
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-I- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                         Phytophthora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X75628; CAA53293.1; ALT_TERM.
HSSP; P02248; 1UBI.
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BIOGENESIS.

SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

MISCELLANEOUS: THIS UBIQUITIN IS SYNTHESIZED &

PRECURSOR WITH 3 EXACT HEAD TO TAIL REPEATS. 7
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Acanthamoeba ubiquitin-fusion
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een the Swiss Institute of Bioinformatics
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Pred. No.
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CONJUGATION TO ACCEPTOR PROTEINS.
D84480E07D1E9B52 CRC64;
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PRINTS; PR00348; UBIQUITIN.
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PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS0053; UBIQUITIN_2; 1.
Nuclear protein; Polyprotein.
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01-FEB-1991 (Rel. 1
01-NOV-1997 (Rel. 3
16-CCT-2001 (Rel. 4
Acyl carrier protei
                                                                                                                                                                               Miyajima N., Hirosawa M., Sugiura M., Sasamoto Hosouchi T., Matsuno A., Muraki A., Nakazaki N. Okumura S., Shimpo S., Takeuchi C., Wada T., Wa Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicell Synechocystis sp. strain PCC6803. II. Sequence entire genome and assignment of potential prote DNA Res. 3:109-136(1996).
 This
                                   "Purification and characterization of acyl cyanobacteria species.";
Eur. J. Biochem. 193:817-825(1990).
-!- FUNCTION: THIS PROTEIN IS THE CARRIER CHAIN IN FAITY ACID BIOSYNPHESIS.
-!- PATHANY: KEY COMPONENT IN DE NOVO FAIT
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka
Kaneko T., Sato S., Kotani H., Tanaka
Miyajima N., Hirosawa M., Sugiura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between
                                                                                                                      MEDLINE=91065389; PubMed=2123456; Froehlich J.E., Poorman R., Reard
                                                                                                                                              SEQUENCE OF 1-61,
STRAIN=ATCC 27184;
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ACPP OR ACP OR SSL2084
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                                                                                                                                                                                                                                                                                                                                  Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrjedes N.C., Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujli C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                           the
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                                                                                                                                                                                                                                           "The complete genome sequence of reducing archaeon Archaeoglobus Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
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ProDom; PD000887; Acyl_carrier; 1.
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                                                                                                                                                                                                                                                                                                                  Venter J.C.
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InterPro; IPR003880; Phosphopant_attach
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                                                               non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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PHOSPHOPANTETHEINE (BY SIMILARITY).
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is fulgidus.";
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EMBL; U56901; AAC44950.1; -.
EMBL; Z99122; CAB15554.1; -.
Subtlist; BG10654; CSFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished observations (SEP-1993).
-!- FUNCTION: COULD ACCELERATE THE C
TRANSCRIPTS POTENTIALLY THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mirel D.B., Chamberlin M.J.;
Mirel D.B., Chamberlin M.J.;
"The Bacillus subtilis flagellin gene
sigma 28 form of RNA polymerase.";
J. Bacteriol. 171:3095-3101(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CSRA FAMILY
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Best Local
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P42740;
01-NOV-1995
01-NOV-1995
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P42739;
01-NOV-1995
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frank S., Menzel D.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION
CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSC
                                                                                  Ubiquitin.
Aglaothamnion neglectum.
Eukaryota; Rhodophyta; Florideophyceae;
Aglaothamnion.
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Eukaryota; Viridiplantae; Ch
Dasycladaceae; Acetabularia.
                      SEQUENCE FROM N.A.
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                                                             NCBI_TaxID=2765;
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MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUI
PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. THERE ARE TW
ADDITIONAL AMINO-ACIDS (ALA-PHE) AFTER THE LAST REPEAT.
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P02248; 1UBI.
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SM00213; UBQ; 1.
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7; Conserv
Grossman
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MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS.
E -> Q (IN ONE OF THE REPEATS).
R -> L (IN ONE OF THE REPEATS).
34D636389D09903F CRC64;
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5; Mismatches
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Pred. No. 89;
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                                                                                                         Ceramiales; Ceramiaceae,
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Best Local S
Matches 8
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P14792;
D1-APR-1990
O1-APR-1990
O1-FEB-1996
Submitted [3]
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VARIANT
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                                    SPECIES=C.elegans; STRAIN-BRISTOL Taich A., Waterston R.;
                                                                                                                 MEDLINE-89181579; PubMed=2538720;
Graham R.W., Jones D., Candidio E.P.M.;
"UbiA, the major polyubiquitin locus in Caenorhabo
unusual structural features and is constitutively
Mol. Cell. Biol. 9:268-277(1989).
                                                                                                                                                                                                                                                                                                                                                       Ubiquitin.
(UBQ-1 OR UBIA OR F25B5.4)
Caenorhabditis elegans, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear
SITE
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                    Geodia cydonium (Sponge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00240; ubiquitin;
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-i- MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
-PRECURSOR WITH SIX HEAD TO TAIL REPEATS. THERE IS ONE ADDITAMINO-ACID (MET) AFTER THE LAST REPEAT.
                                                                                                                                                                                                                                                                             NCBI_TaxID=6239,
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P02248; 1UBI.
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8; Conser
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CONJUGATION TO ACCEPTOR PROTEINS
L -> I (IN ONE OF THE REPEATS).
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I -> L (IN ONE OF THE REPEATS).
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locus in Caenorhabditis
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Best Local
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EMBL; U23172; AAC44552.1; A
EMBL; M21321; AAA28153.1; -
EMBL; L31492; AAC37252.1; A
EMBL; X70917; CAA50268.1; A
PIR; A30126; A30126.
PIR; A30126; A30126.
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NOT; SM00212
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                   BINDING
SEQUENCE
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J. Cell Sci. 106:545-554(1993).

-!- FUNCTION: INVOLVED IN THE ATD-DEPENDENT SELECTIVE DEGRADATION CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batel R., Mueller I.M., Mueller E.W., Cloning of the polyubiquitin cDNA from the marine sponge Geodia "Cloning of the polyubiquitin cDNA from the marine sponge Geodia of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graham R.W., van Doren K., Bektesh S., Candido E.P.M.; "Maturation of the major ubiquitin gene transcript in Caenorh elegans involves the acquisition of a trans-spliced leader."; J. Biol. Chem. 263:10415-10419(1988).
                                                                                                                                                                                                                                                  WormPep; F25B5.4; CE01921.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfeifer K., Frank K., Schroeder H.C., Batel R., Mueller I.M., Mueller E.G.;
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MEDLINE=94110294; PubMed=8282761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=C.elegans; STRAIN=BRISTOI MEDLINE=96018742; PubMed=7556908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (UBQ-2).
SPECIES=C.elegans; STRAIN=BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-37 FROM N.A. SPECIES=C.elegans;
                                                                                                                                                                                         PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH 11 EXACT HEAD TO TAIL REPEATS. THERE ARE TW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDITIONAL AMINO-ACIDS (ASP-ILE) AFTER THE LAST REPEAT.
                          GETFQVEVPGSQHIDSQKKAI
GKTITLEVEASDTIENVKAKI
                                                                                                                                                                                                                                                                                               P02248; 1UBI
                                                       Similarity 38.8; Conservative
                                                                                                                                                                            protein;
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SM00213; UBQ; 1.
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AA;
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                                                                                                                                                              Polyprotein.
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8539 MW;
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38.1%;
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ALT_TERM.
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ALT_TERM.
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                                                                     Score 34;
Pred. No.
                                                                                                               MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS
C43B24396EEC9B52 CRC64;
                                                                                                                                                              NECESSARY FOR BRANCHED-CHAIN
                                                      Mismatches
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89;
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P14624;
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01-APR-1990
01-NOV-1997
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EMBL; X60826; CAA43216.1;
PIR; S06598; UQKM.
HSSP; P02248; IUBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00240; ubiquitin; 1
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
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Eur. J. Biochem. 202:197-204(1991)
-!- FUNCTION: INVOLVED IN THE ATP-
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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MEDLINE=92037644; PubMed=1657605;
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SITE 48 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POllmann L., von Kampen J., Wettern M.; "Ubiquitin in a lower plant. Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=2137
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SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
MISCELLANEOUS: UBI1 IS SYNTHESIZED AS A POLYPROTEIN WITH
OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSC
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CONJUGATION TO ACCEPTOR PROTEINS C42936277D1E9B52 CRC64;
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"Genomic and transcriptional linkage of the genes for calmodulin, hand 5 protein, and ubiquitin extension protein 52 in Trypanosoma brucel.";
MOI. Cell. Biol. 13:207-216(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-90136711; PubMed-2559328;
Wong S., Campbell D.A.;
"A polyubiquitin gene from Trypanosoma brucei.";
"A polyubiquitin gene from Trypanosoma brucei.";
"A polyubiquitin gene from Trypanosoma brucei.";
                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=427;
MEDLINE=91083842; PubMed=2175891;
Wong S., Morales T.H., Campbell D.A.;
"Ublquitin-EP52 fusion protein homologs from Trypanosoma brucei.";
Nucleic Acids Res. 18:7181-7181(1990).
                                                                                                                                                                                                                                                                                                                                EMBL; X14554; CAA32691.1; ALT_TERM.
EMBL; X54641; CAA38453.1; -.
EMBL; X54642; CAA38454.1; -.
EMBL; X56511; CAA39863.1; -.
EMBL; X56511; CAA39864.1; -.
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PIR; S14197; S14197.
HSSP; P02248; 1UBI.
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PROSITE; PS50053; UBIQUITIN_2; 1.
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SUBCELLAURAE LOCATION: Nuclear and cytoplasmic.
SUBCELLAURAEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
MISCELLANGOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH 5 OR 6 EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN
GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL
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FUNCTION: INVOLVED IN THE AFF-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
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GKTIALEVEASDTIENVKAKI
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CONJUGATION TO ACCEPTOR PROTEINS.
C53759576F0C8E47 CRC64;
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sp_rvirus:*
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Q97QB1
Q97P24
                                                                                                                                                                        SUMMARIES
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(without alignments)
148.629 Million cell updates/sec
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O9syf4 arabidopsis
O97g4b streptococc
O97g2b streptococc
O97g2b streptococc
O9m4a4 cucumis mel
O36044 mastigamoeb
O07188 saccharomyc
O36058 mastigamoeb
O39y18 rattus norv
O9gy18 rattus norv
O9gi64 campylobact
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O9si62 zea mays (m
O42009 arabidopsis
O42001 arabidopsis
O42001 arabidopsis
O9m646 oryva sattiv
O94im2 medicago tr
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ALIGNMENTS

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ID Q9SYF

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Matches 10
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SYSAIN-CV. COLUMBIA;

Yysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C.,

Li J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Alt

Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.

Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,

Davis R. W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC FISII sequence.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AC006571; AAD25769.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SYF4 PRELIMINARY; PRT;
Q9SYF4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last seq
Q1-DEC-2001 (TrEMBLrel. 19, Last ann)
                                                                                                                                                                                                                                                                               HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 2.
SEQUENCE 91 AA; 10142 MW; E
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
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F15I1.6.
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                                                                     1 GETFQVEVPGSQHIDSQKKAI
GKTFNLEVKGSEIIQQVKNMI 78
                                                                                                                                               1 Similarity
10; Conserv
                                                                                                                                                   Conservative
                                                                                                                                                                                  43.0%;
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                                                                                                                                               Score 46; DB Pred. No. 3.8; 3; Mismatches
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Q97PZ4;
Q1-OCT-2001
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01-DEC-2001
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Q97QB1;
Q1-QCT-2001
Q1-QCT-2001
Q1-DEC-2001
IS66 FAMILY
                                                                                  Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., Hctzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey F. Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                             STRAIN-TIGR4;
MEDLINE-21357209; PubMed-11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
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NCBI_TaxID=1313;
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TIGR; SP1314; -.
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Streptococcus pneumoniae.
                                                                        Science
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Science 293
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                      Ce 293:498-506(2001).
AE007441; AAK75537.1;
SP1443; -.
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E007429; AAK75412.1;
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proteome
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PROSITE;
                                                                     and Psalteriomonas lanterna: Ph
Submitted (JUL-1997) to the EMB
EMBL; AJ000658; CAA04206.1; -.
HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                       Mastigamoeba balamuthi.
Eukaryota; Pelobiontida;
NCBI_TaxID=108607;
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; I
Spermatophyta; Magnoliophyta; eudicotylec
eurosids I; Cucurbitales; Cucurbitaceae;
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01-OCT-2000 (TremBLrel. 15,
01-DEC-2001 (TremBLrel. 19,
PUTATIVE RESISTANCE GENE HON
                                  PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                     SEQUENCE FROM N.A. Woestmann C., Hack
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26 VEIPQSRRFDSKKR
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int Sci. 161:165-172(2001)

3L; AJ251872; CAB88871.1; --

terPro; IPR002182; NB-ARC.
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UBIQUITIN_2;
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10139 MW;
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                                                                                                                                                                                                                                                                           Mastigamoebidae;
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                                                                                                                                                                                                                                                                                                                                            O36058; PRELIMINARY;
O36058; O1-JAN-1998 (TrEMBLrel. (
O1-JAN-1998 (TrEMBLrel. (
O1-DEC_2001 (TrEMBLrel. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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SEQUENCE
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Submitted
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                 EMBL;
EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyubiquitin precursor protein.";
Nature 312:663-666(1984).
EMBL; X01473; CAA25705.1; -.
HSSP, P02248; UBI4.
SGD; S0003962; UBI4.
InterPro; IPR000626; Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85061630; PubMed-6095120;
Oezkaynak E., Finley D., Varshavsky A.;
"The yeast ubiquitin gene: head-to-tail
                                                                                                                                                                                                                                                                                                                              UBIQUITIN (FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00240; ubiquitin; 1. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   007188
                                                                                                                                                                                                                                                     Eukaryota; Pelobiontida; NCBI_TaxID=108607;
                                                                                                                                                                                                                                                                                                 Mastigamoeba balamuthi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Pfam; PF00240;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                            ttmann C., Hackstein J., Bakl
iitted (JUL-1997) to the EMBI
J. AJ000656; CAA04204 1; -
J. AJ000656; CAA04208 1; -
J. AJ000655; CAA04203 1; -
J. AJ000655; CAA04207 1; -
J. AJ000659; CAA04207 1; -
J. AJ000659; CAA04207 1; -
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47 AA; 5220 MW; B
                  IPR000626; Ubiquitin
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Pred. No.
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01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                           O9QYJ8 PRELIMINARY; PRT; 77 AA.

Q9QYJ8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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STRAIN=WISTARST;
MEDLINE-20130146; PubMed-10663575;
Miwa T., Okada N., Okada H.;
                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                036043
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NON_TER 1
NON_TER 62
                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                 DECAY ACCELERATING FACTOR (FRAGMENT).
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                                                                    SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GKTITLEVEPSDSIDNVKQKI
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Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat

Rattus.

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woestmann C., Hackstein J., Bakker-Grunwald T.;
"Ubiquitin sequences and polyubiquitin genes in Phreatamoeba
and Psalteriomonas lanterna: Phylogenetic implications.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ000657; CAA04205.1;
HSSP; P02248; 10B1.
InterPro; IPR000626; Ubiquitin.
                                                                                                                      PROSITE; PS00299; UBIQUITIN_1; PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                 PRINTS; PR00348; UBIQUITIN. SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0348; UBIQUITIN.
SMART; SMO0213; UBC; 1.
PROSITE; PS00299; UBIQUITIN_1;
PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                                               Mastigamoeba balamuthi.
Eukaryota; Pelobiontida;
                                                                                                                                                                                                                                                                                                                                                           UBIQUITIN (FRAGMENT).
                                                                                                                                                                            Pfam; PF00240; ubiquitin;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=108607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GETFQVEVPGSQHIDSQKKAI
1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKTITLEVEPSDSIDNVKQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; PR00348; UBIQUITIN.
SM00213; UBQ; 1.
                           Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
9; Conserv
                                                                              62 AA;
                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.)
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                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6978
                                                                               6906 MW;
                                      36.4%;
42.9%;
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21
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 37;
4; Mismatches
                                         Score 39;
Pred. No.
                                                                               7C14EEC0F3B19D20 CRC64;
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                           Mismatches
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37;
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RESULT
Q9SAT2
ID Q9
AC Q9
DT 01
DT 01
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DT 01
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Q9SAT2 PRI
Q9SAT2;
01-MAY-2000 (TI
01-MAY-2000 (TI
01-DEC-2001 (TI
POLYUBIQUITIN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PI64;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-DEC-2001 (TrEMBLrel. 19, L
ACYL CARRIER PROTEIN (ACP)
ACPP OR CJ0441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Wren B.W., Mungall K., Ketley J.M., (Parkhill J., Wren B.W., Mungall K., Ketley J.M., (Basham D., Chillingworth T., Davies R.M., Feltwell Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Ouail M.A., Rajandream M.A., Rutherford K.M., van Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003231; Acyl_carrier.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF005500; pp-binding; 1.
ProDom; PD000887; Acyl_carrier; 1.
PROSITE; PS0075; ACP_DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
COMPLETE PS00012; PHOSPHOPANTETHEINE; 1.
SEQUENCE 77 AA; 8598 MW; 772D693BDC89588F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylphophatidylinositol-anchored and transmembrane forms of rat decay-accelerating factor.";
Immunogenetics 51:129-137(2000).
EMBL; AB026905; BAA88994.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni.
Bacteria; Proteobacteria;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: THIS PROTEIN IS THE CAN
CHAIN IN FATTY ACID BIOSYNTHESIS
EMBL; AL139075; CAB74277.1; -
HSSP; P02901; 1ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-NCTC 11168; MEDLINE-20150912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reveals hypervariable sequences."; Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-197;
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10; Conserv
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Similarity 35.3%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
  (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
IN HOMOLOG (FRAGMENT).
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Conservative
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33.3%;
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Pred. No. 47;
4; Mismatches
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Last annotation update)
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ESIS (BY S
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Il T., Holroyd S
, Penn C.W.,
n Vliet A.H.M.,
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AC AC

Q42001 Q42001;

PRELIMINARY;

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RESULT 13
Q42001
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ID 04200
AC 04200
AC 04200
AC 01-NC
DT 11-NC
RN 111
RP SEQUE
RC MASH
DR HSSP;
DR INSSP;
DR INSSP;
DR INCN
DR SARNI
DR Pfam;
DR Pfam;
DR Pfam;
DR SNARNI
DR SNA
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Best Local S
Matches
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Best Local
                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Mache R., Quigley F., Thomas F., Submitted (NOV-1992) to the EMBL, EMBL; 218425; CAA79186.1; -. HSSP; P02248; IUBI. InterPro; IPR000626; Ubiquitin. Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              PRINTS;
SMART;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S82312; AA847174.1; -.
HSSP; P02248; 1UBI:
InterPro; IPR000626; Ubiquitin.
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                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50053; UBIQUITIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=FLOWER BUDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UBIQUITIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q42009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00240; ubiquitin; 1 PRINTS; PR00348; UBIQUITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Didierjean L., Frendo P., Nasser "Heavy-metal-responsive genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
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SM00213; UBQ;
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9; Conserv
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9; Conserv
                                                                                                                                                                                                                                                                      52 AA;
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                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                    5914 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.THALIANA ECOTYPE COLUMBIA C24;
Thomas F., Yu DY.;
to the EMBL/GenBank/DDBJ databases.
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Pred. No. 44;
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Pred. No.
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31;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

UBIQUITIN (FRAGMENT).

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Q9M64 PAGE ID Q9M64 AC Q9M64 AC Q9M64 AC Q9M64 PG O1-OC DT 01-DE DE UBIQUO OS OFFER AC TISSUE RN [1] RP SEQUE RC TISSUE RT Lissue RL Submitor RT Lissue RL Submitor RT Lissue RL Submitor RT Total Submitor RT Sub
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UBIQUITIN RIP-20 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-FLOWER BUDS OF A.THALIANA ECOTYPE COLUMBIA C24; Mache R., Quigley F., Thomas F., Yu DY.; Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases EMBL; Z18379; CAA79175.1; -. HSSP; P02248; 1UBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                     PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBIQUITIN_1;
                                                                                                                                                                                                                                                                                                                                                 HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=PANICLE;
Sheotran I.S., Saxena D., Saini H.S.;
Expression of drought-responsive ubiquitin genes in reproductive tissues of rice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF216530; AAF37225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
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Pfam; PF00240; ubiquitin; 2.
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GKTITLEVESSDTIDNVKAKI 25
                                                                                                Similarity 42.9
9; Conservative
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9; Conserv
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5918 MW;
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Pred. No. 64;
3; Mismatches
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Pred. No. 46;
3; Mismatches
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RESULT 15

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Q94IM2
AC Q99
AC Q90
AC Q90
DT Q1
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AC Q90

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Search completed: October 24, Job time: 25.4426 secs
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Medicago truncatula (Barrel medic).

Medicago truncatula (Barrel medic).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae

Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae; Medicago.
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Q94IM2;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Plant Microbe Interact. 13:763-777(2000). EMBL; AJ245511; CAB96875.1; -. NON_TER 76 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20331592; PubMed=10875337; Salzer P., Bonanomi A., Beyer K., Voegeli-Lange R., Aeschbach Lange J., Wiemken A., Kim D., Cook D.R., Boller T.; "Differential expression of eight chitinase genes in Medicago truncatula roots during mycorrhiza formation, nodulation and infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                      15:36:53
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Recombinant exotox Labile toxin (LT-B C. jejuni flagelli Cholera toxin B/en Synthetic cholera Heat labile entero

Recombinant Recombinant Recombinant exotos

exotox exotox

Cholera toxin B su

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Title:
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107
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2: \SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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Copyright (c) 1993 - 2002 Compugen
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Amino acid sequence V. cholera cholera V. cholera cholera V. cholera cholera V. cholera Toxin B-su E. coli LTB protei B subunit of the h Cholera toxin B su Amino acid sequence Plant-optimized E. Cholera toxin B su V. cholera cholera Strain V. cholera cholera V. cholera Cholera

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Derivatives of Escherichia coli heat labile enterotoxins useful as fimmunomodulators and for treating diarrhea and which do not bind figlycolipid receptor GM-1 -	WPI; 2000-256943/22.	X Williams NA, Hirst TR;	(UYBR-) UNIV BRISTOL.	R 07-SEP-1998; 98GB-0019484.	7 7 7 7 7 8 7 9 9 9 9 9 9 9 9 9 9 9 9 9	0 16-MAR-2000.	N WOZUUU14I14-A1.		s Escherichia coli.		w beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;			F coli heat labile enterotoxin R-derived neptide. SEO ID NO:5	T 03-JUL-2000 (first entry)		C AAY87463;	F - F	TD AAV87463 standard: nontide: 21 AA	RESULT 1

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AAY87463 AAR72545 AAY41816 AAW95226 AAW95239 AAB662379 AAB662377 AAB62377

E. coli heat labil
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Best Local
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 Disclosure;
                                        New modified forms of pertussis holotoxin - crystalline forms of pertussis holotoxin and
                                other molecules
                                                                                                                   Armstrong GD,
Oomen R, Read
                                                                                         WPI; 1995-132623/18.
                                                                                                                                                                (CONN-) CONNAUGHT LAB LTD (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                             24-AUG-1993;
31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                               Bacteria sp
                                                                                                                                                                                                                                                                                                                                                                              Bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP-ribosylating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to peptide fragments of the Escherichia coli heat
lle enterotoxin (Etx) and its closely related homologue, cholera
in (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
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llarity 100.0%;
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                                                                                                                   Cockle SA,
RJ, Stein
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94US-0251121
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54pp;
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 English
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Pred. No. 2.6e-11;
Mismatches 0;
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RESULT 3
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CC involving analysis of the 3-dimensional form of the crystalline cholotoxin. The pertussis holotoxin modification process comprises: CC (1) identification of at least one amino acid (aa) residue of the crystalline cc (1) identification of at least one amino acid (aa) residue of the ccystalline holotoxin, in relation to known information of the protein ct crystalline holotoxin, in relation to known information of the protein ct curvature and function; (2) effecting mutagenesis (by removing or cc replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa)
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd, from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-579908/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method for producing modified pertussis holotoxin
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The invention relates to methods of preparing a pertussis holotoxin (PT)
C having a modified biological activity. One method comprises identifying
at least 1 site in a PT that interacts with a molecule that is capable of
forming a complex with the holotoxin and which molecule is an effector
molecule which is an adenine nucleotide and which site contributes to
toxicity, cell binding or enzymatic activity of PT. The functional
interacting site(s) are identified by analysing the three dimensional
structure of crystalline PT, determined by X-ray crystallogaphy. The
identified interacting site(s) are modified to alter toxicity, cell
binding or enzyme activity of the PT. The methods can be used to alter a
biological activity such as toxicity, enzymatic activity, mitogenicity,
cell binding and adjuvanticity of the PT. The three-dimensional structure
of PT have functional and/or structural resemblance to other bacterial
toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the
heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating because the present in the exemplification of the present product that the present product is the present product that the present product the present product
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No. 1.5e-10;
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24-AUG-1993;
31-MAY-1994;
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Hazes B,
                                                                                                           pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAV68340 to AAV68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crystalline for proteins which
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Matches

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Mismatches

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Indels

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Gaps

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Conservative

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ID ARAB66239
ID ARAB6
XX ARAB6
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XX Pert
KW Pert
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OX Esch
XX V
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ID AAB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
  29-JUN-2001
                          AAB62379;
                                                  AAB62379
                                                                                                                                                                                                                                                                                                                                                                                                 Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify of toxicity, cell binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                         Example
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Stein PE;
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                        41pp; English.
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                                                                                                                                                                  Score 107; DB 22;
Pred. No. 1.5e-10;
Mismatches 0;
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histamine-sensitising factor;
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The invention relates to a recombinant AB5B subunit protein comprising at least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cystelnes to an immunogen or vaccine. Recombinant mutant CTB (rCTB) can be used in the treatment of autoimmune diseases e.g. Theumatoid arthritis, encephalomyelitis (or other neuron constitute of a constant and diseases e.g. Theumatoid arthritis, encephalomyelitis (or other neuron constant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; LTB infection; parasitic; immunosuppressive; antiarthitic; antirheumatic; antidiabetic; neuroprotective; vaccine; heat labile toxin B; variant.
                                                       demyelinating diseases) and diabetes. The rCTB or other B subunits invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a variant of t
                                                                                                                                                                                                                                                                                                                                                                                          Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
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                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                      coli heat labile toxin B (LTB) protein
                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases
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                                                          The present sequence represents a variant of the
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GETFQVEVPGSQHIDSQKKAI
                                        Similarity
                                 Conservative
                                        100.0%;
65
                                 0;
                                Score 107; DB 22; Pred. No. 1.7e-10; Mismatches 0;
                                               Length
                                 Indels
                                                  103;
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Sequence

103 AA;

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RESULT 8
AAB62377
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX 29-J
XX E. C
XX AB5E
KW Infec
KW Infec
KW Infec
XX AB5E
XX SESC!
XX ESC!
                                                                                     29-JUN-2001
                                                                                                      AAB62377;
                                                                                                                      AAB62377 standard;
                                                                   coli LTB protein
                                                                                    (first
                                                                                                                     Protein;
                                                                                    entry)
                                                                    variant
                                                                                                                       123
                                                                    (GI:
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AB5B subunit protein; immunogen; autoimmune infection; parasitic; antidiabetic; neuropro Escherichia coli neuroprotective; mutation; recombinant; cholera toxin B; CTB; disease; neuron demyelinating disease; rCTB; LTB immunosuppressive; antiarthritic; antirheumatic; otective; vaccine; heat labile toxin B; variant.

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RESULT 9
AAB62373
ID AAB6
XX AAB6
XX AAB6
XX AAB6
XX E. C.
XX AB5B
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KW inmum
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                                                                                                                                                                                                                                                                                                                                                                   AB5B subunit protein; mutation; recombinant; choiera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; LTB infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; heat labile toxin B; variant.
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                                                                                                                                                                                                                                                           WO200127144-A2
                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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RESULT 10
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XX AAB6;
XX AAB5;
XW AAB5;
XW AAB5;
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                                                                                                                                                                                                                                                                                            (ACTI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200127144-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogen;
infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB5B subunit protein;
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                                                                                                                                                                                                                                                                                               ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasitic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haaparanta
                                                                                                                                                                                                                                           Haaparanta T,
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                                                                                                                                                                                                                                                                                               BIOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation; recombinant; under disedisease; neuron demyelinating dise immunosuppressive; antiarthritic; heat labile tox:
                                                                                                                                                                                                                                                                                               AΒ
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Pred. No. 2.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; heat labile toxin B; variant.
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Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for

Disclosure; Page 71;

78pp; English.

treating autoimmune diseases

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              The invention relates to a recombinant AB5B subunit protein comprising least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a will type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (rCTB) can be used in the treatment of autoimmunum and the contraction of the covalence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; heat labile toxin B; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant AB5B subunit protein comprising at least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (rCTB) can be used in the treatment of autoimmune diseases e.g. rheumatoid arthritis, encephalomyelitis (or other neuron and diseases).
                                                                                                                                                                                                                                                                                covalently linking to an immunogen treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                               number residues available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACTI-) ACTIVE BIOTECH
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                                                                                                                                                                                                                                    Page 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                 English.
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Pred. No. 2.1e-10;
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                 to an immunogen or vaccine. in the treatment of autoimmune
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                                                                                    The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heart-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                               Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           demyelinating diseases) and diabetes. The rCTB or other B subunits of invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a variant of the E. coli heat labile toxin B (LTB) protein.
                                                  Sequence
                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding an exotoxin and a nucleic acid affinity domain -
  Exotoxin mucosal cell binding nucleic acid affinity domain;
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                                                                                  Recombinant exotoxin
                                                                                                                                        14-MAY-2001
                                                                                                                                                                                               AAB73243;
                                                                                                                                                                                                                                               AAB73243 standard; Protein; 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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21; Conserv
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                                                                                                                                        (first entry)
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                                                                                  variant LTB-P.
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motif; nucleic acid delivery;
heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107; DB 22;
Pred. No. 2.5e-10;
; Mismatches 0;
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heat-labile enterotoxin.
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                                                                                                                                                         18-AUG-2000;
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DB; AAF75714.
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                                                                                                                                                                                                                                           Sequence
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N-PSDB; AAF75715.
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US-08-952-337-5
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US-09-11852-21
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US-08-747-410-2
US-08-952-337-2
US-08-449-045C-4
US-08-878-989-2
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Sequence 35, Appl	Sequence 35, Appl	Sequence 5, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 133, App	Sequence 133, App	Sequence 2, Appli	Sequence 30, Appl	Sequence 23, Appl	Sequence 2, Appli				

ALIGNMENTS

PRIOR APPLICATION: 435
PRIOR APPLICATION UMBER: US 08/110
FILING DATE: 24-AUG-1993
PRIOR APPLICATION UMBER: US 08/251
FILING DATE: 31-MAY-1994
PRIOR APPLICATION UMBER: US 08/251
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26: GENERAL INFORMATION:
APPLICANT: READ, Randy J. SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: TITLE OF INVENTION: MODIFICATION OF NUMBER OF SEQUENCES: 46 ADDRESSEE: Sim (
STREET: Suite 70
CITY: Toronto
STATE: Ontario FILING DATE: 26, ... 5856122 TRY: Canada M5G 1R7 Application US/08292968 E: Sim & McBurney Suite 701, 330 Un COCKLE, Stephen A OOMEN, Raymond P. HAZES, Bart LOOSMORE, Sheena KLEIN, Michel H. ARMSTRONG, Glen STEIN, Penelope US 08/251,121 08/110,947 University Avenue 1038-388 D PERTUSSIS

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                       REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 06-JUN-1995
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FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 31-MAY-1994
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                                           Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
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ZIP: M5G 1R7
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                                                                                                                                               93 amino acids
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Suite 701, 330 University Avenue
                                                                                                                                                                           (416) 595-1163
(77) TD NO: 26:
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                          Score 107; DB 2;
Pred. No. 2.7e-11;
; Mismatches 0;
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Pred. No. 2.7e-11;
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US-08-467-976-26
; Sequence 26, Application US/08467976
; Patent No. 6018022
; GENERAL INFORMATION:
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US-08-467-536-26
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                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0: FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                   35 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                              LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite
CITY: Toronto
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                                                                                                                               1 GETFQVEVPGSQHIDSQKKAI 21
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NO. 5977304
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M5G 1R7
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21; Conserv
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SYSTEM: PC-DOS/MS-DOS
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ite 701, 330 University Avenue
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31-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                      us 08/110,947
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                                                                                                                                                                                                                                                                                                                                                               1038-455 MIS:vg
                                                                                                                                                                        Score 107; DB 2;
Pred. No. 2.7e-11;
                                                                                                                                                            Mismatches
                                                                                                                                                                                       Length 93;
                                                                                                                                                            Indels
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                                                                                                                                                                   Sequence 26, Application US/09082514 Patent No. 6168928
                                                                          GENERAL INFORMATION:
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-JUN-139J
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US 08/292,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAZES, BATITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,
                                                                   APPLICANT:
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 UMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 01 FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FTI.ING DATE: 24-AUG-1993
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                                                                                                                                                                                                                                                                                            1 GETFQVEVPGSQHIDSQKKAI 21
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                   INVENTION:
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Suite 701, 330 Un
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                               KLEIN, Michel H. ARMSTRONG, Glen D.
                                 HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAZES, Bart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOOSMORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             READ, Randy J.
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODIFICATION OF PERTUSSIS TOXIN
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MODIFICATION OF PERTUSSIS TOXIN 46
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                                                                                                                                                                                                                                                                                                                                                                          Length 93;
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RESULT 6
US-08-829-026A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08829026A Patent No. 5837825
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ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

THE PC-DOS/MS-DOS

THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                   SOFTWARE: PatentIn Rela
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US;
FILING DATE: 18-AUG-19:
CLASSIFICATION: 435
                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 24-AUG-1994
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ADDRESSEE: Sim & McBurney
                                 ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6th F1
CITY: Toronto
                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Graeter, Janelle S. REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 01
                   NAME: Graeter, Janel REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                           STREET: Room 411,
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                              Janelle S. Graeter
                                                                                                                                                                                         Floppy disk
                                                                                     18-AUG-1997
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                                                                                                       US/08/829,026A
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RESULT 8
US-08-952-337-6
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; DRCANISM: Vibrio cholerae
US-08-952-337-5
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Best Local Similarity 100.
Thes 21; Conservative
             NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 102
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08952337 Patent No. 6019973
                                                                                  TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: ECT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1995-05-05
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE TITLE OF INVENTION: ENPEROTOXIN AND CHOLERA TOXIN B SUBUNITS FILE REFERENCE: 3846/00758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1998-01-05

EARLIER FILING DATE: 1996-05-02

EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                        APPLICANT: Holmgren, Jan APPLICANT: Lebens, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER FILING DATE: 1995-05-05
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                          44 GATFQVEVPGSQHIDSQKKAI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHIDSQKKAI 21
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95.2%;
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Pred. No. 1.5e-10;
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 3;
Pred. No. 3.3e-10;
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RESULT 10
US-08-894-526-2
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                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-472-171-2
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                                                                                                                                 Matches
                                                                                                                                                Query Match
Best Local :
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEFAX: 416-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
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                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                 45 GATFQVEVPGSQHIDSQKKAI
                                                                                                                               Local Similarity 95.: es 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 23-FEB-1995
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CITY: Toronto
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                                                                                               1 GETFQVEVPGSQHIDSQKKAI 21
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M5G 1R7
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330 University Avenue, Suite 701
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                                                                                                                                              94.48;
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Pred. No. 3.3e-10;
0; Mismatches 1;
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                                                                                                                                                               Length 103;
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Sequence 2, Application US/08894526 Patent No. 5942418 GENERAL INFORMATION:

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Query Match
Best Local Similarity
"atches 20; Conserv
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Patent No.
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                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STATE: Ontario
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                                                                                                          ZIP: M5G 1R7
                                                                                                                                                                       STREET:
                                                                                                                                                          CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                               45 GATFQVEVPGSQHIDSQKKAI 65
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 APPLICATION NUMBER:
                                                                                                                             COUNTRY:
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amino acid
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Zealey, Gavin R.
Klein, Michel H.
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Klein, Michel H
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                                                                                                                                                                                                                                    Expression Of Gene Products From Genetically Manipulated Strains (
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US/09/013,047
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Pred. No. 3.3e-10;
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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 REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FEBRUAR
                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                    COUNTRY: Canada
ZIP: M5G 1R7
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TELEPHONE:
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Zealey, Gavin R.
Klein, Michel H.
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                                                                                                                                                                                                                                                                                                                                                                                                      Sim & McBurney
                                                                                                                FEBRUARY 23, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression Of Gene Products From Genetically Manipulated Strains Of Bordetella
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95.28;
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                                                                                                                                     08/393,334
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Pred. No. 3.3e-10;
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RESULT 14
PCT-US95-13376-21; Sequence 21, App
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US-09-191-852-21
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                                                                                                                                                             Matches
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Best Local Similarity
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Sequence 21, Application PC/TUS9513376 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                              45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fox, David L.
REGISTRATION NUMBER: 40,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/191,852 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TX
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
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Local Similarity 95.2%;
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                                                                                                                                                                                                                                       i: 103 amino acids
amino acid
DGY: linear
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                                                                                                                                                                            Score 101; DB 4; Length 103; Pred. No. 3.3e-10;
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Pred. No. 3.3e-10;
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; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-08-952-337-1
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US-08-952-337-1
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                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08952337 Patent No. 6019973
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER FILING DATE: 1995-05-05
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APPLICATION NUMBER: US 08/328
APPLICATION NUMBER: US 08/328
ATTORNEY/AGENT INFORMATION:
NAME: JONES, JOHN W.
REGISTRATION NUMBER: 31,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           LENGTH:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
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TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GATFQVEVPGSQHIDSQKKAI 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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   94.4%;
95.2%;
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   Score 101; DB 3; Pred. No. 4.1e-10;
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Search completed: October 24, 2002, 15:24:00 Job time : 13.3934 secs	1 GETFQVEVPGSQHIDSQKKAI 21 	20; Conservative 0; Mismatches
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15:24:00		Mismatches
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                Score
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Match
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                                                                                                                                                                                                Length DB
         1 US-09-786-648-5

US-08-110-947-10

US-08-110-9478-26

US-08-251-121-26

US-08-251-121-26

US-08-784-218-358-3

1 US-08-774-218-65

2 US-08-829-026-5
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Sequence 5, Appli
Sequence 10, Appl
Sequence 26, Appl
Sequence 26, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 5, Appli
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45	44	43	42	41	40	39	38	37	36	35	34		32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ
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08-427-58	-09-252-991A-	-09-252-691C-692	-09-252-691-69	-09-689-980-80	-09-391-631-31	-689-980-	US-09-391-631-3104	-451-320-	63-997-	-09-769-970-	-09-7	-09-786	-08-7	-08-732	-09-402	-09-402-100-	423-493-	-09-051-31	-US01-08582-	-US01-08582-	-09-760-234-	-09-470-124-5	-US99-30747-5	-09-756-983-	-09-756-983-1	-09-756-983	-08-914-479A-	-08-914-479-2	-09-470-124-5	-US99-30747-	-09-836-433-2	-09-836-433-2	-09-836-433-1	S-08-817-906-2	S-08-782-832-1	08-393-3	US-09-786-648-4
5824	equence 292	6923,	6923,	801, 7	3103,	802, 1	3104,	388, 1	4,	2,	415	ω	1,	1,	4,	Ņ	2	رة ق	4,	3, AI	7,	e 57,	57, P	22,	equence 18,	equence 15,	equence 2, Appl	2, Appl	e 55,	quence 55, A	equence 22,	20,	equence 14,	21,	e 15	2, Appl	Sequence 4, Appli

ALIGNMENTS

RESULT 1 US-09-786-648-5

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GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccing Title OF INVENTION: Adjuvants
FILE REFERENCE: 7438
FILE REFERENCE: 7438
                                           Matches
                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                   SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
                                                                                                                                       LOCATION: 45...65
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivabl
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: E. coli
FEATURE:
                                                                                                                                                                                                                                                            LENGTH: 21
1 GETFQVEVPGSQHIDSQKKAI 21
                                                             Similarity
                                         Conservative
                                       100.0%; Score 107; DB 21; 100.0%; Pred. No. 1.4e-10; o, mismatches 0;
                                           Indels
                                                                              Length
                                                                                  21;
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                                           Gaps
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RESULT 3
US-08-110-947A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
TELEEX: 899456 LUKPAT
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           Sequence 26, Application US/08110947A GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                        APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                   NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/00
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FAILOW Charles W
                                                                                       TITLE OF INVENTION:
                                                                                                         APPLICANT:
                                                                                                                                                            APPLICANT:
                                                                                                                                                                           APPLICANT: READ, Randy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 22202-0286
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                    GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                    GETFOVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08110947
E: Shoemaker and Mattare, Ltd.
Suite 1203 Crystal Plaza I, 2001 Jefferson
Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 1203 Crystal Plaza I, 2001 Jefferson Davis Hwy.
                                                                                                      OOMEN, Raymond P
KLEIN, Michel H
                                                                                                                                        COCKLE, Stephen A
                                                                                                                                                       STEIN, Penelope E
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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KLEIN, Michel H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                       MODIFICATION OF PERTUSSIS TOXIN
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Matches
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                                              FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 46
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         STREET: Suite CITY: Toronto
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5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                 NAME:
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                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                       TRY: Canada
M5G 1R7
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21; Conserv
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                                STEWART, Michael
                                                                                                                                                                                                                                                                                                           Ontario
                                                                                                                                                                                                                                                                                                                                           Suite 701,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 107; DB 5; llarity 100.0%; Pred. No. 9.3e-10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      READ, Randy J
                                                                                                                                                                                                                                                                                                                                                                                                                                               ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                             Sim & McBurney
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 NUMBER:
                                                                                                                                                                                                                                                                                                                                           330 University Avenue
                                                                                                                                                  US/08/251,121
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              24,973
1038-335
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                                                                                                                                                                                       Version #1.25
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RESULT 6
US-08-784-218-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Sequence 6, Application US/08784218 GENERAL INFORMATION:
                                                                                                                                                                            Matches
                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,305A
FILING DATE: 12-NOV-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: CAMPYLOBACTER JEJUNI
TITLE OF INVENTION: FLAGELLIN-ESCHERICHIA COLI ST-B FUSION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                              MOLECULE TYPE: protein 150-305A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Meinersmann, Richard J. APPLICANT: Khoury, Christian A.
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Beltsville
                                                                                                      49 GETFQVEVPGSQHIDSQKKAI 69
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Graeter, Janelle S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
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)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 107; DB 6; ilarity 100.0%; Pred. No. 9.3e-10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       202-504-5060
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Janelle S. Graeter
com 413, Building 005, BARC-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                        100.0%; Score 107; DB 5;
100.0%; Pred. No. 5.5e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                           Length 371;
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; MOLECULE TYPE: protein US-08-784-218-6
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 18-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Meinersmann, Richard
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: CampylobacturiTITLE OF INVENTION: Flagellin-E
                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Meinersmann, Richard J. APPLICANT: Khoury, Christian A. TITLE OF INVENTION: Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                      COUNTRY: US
ZIP: 20705
                                                                                                                                                                                                                                                        CITY: Beltsville
STATE: MD
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nes 21; Conserv
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            NAME: Graeter, Janelle S. REGISTRATION NUMBER: 35,024
                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                    MEDIUM TYPE:
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Room 411, Building 005, BARC-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Janelle S. Graeter
Room 411, Building 005, BARC-W
                                                                                                                                                                                                                                        USA
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Pred. No. 5.5e-09;
; Mismatches 0;
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Floppy disk

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US-08-393-334-2
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US-09-786-648-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILLING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 301-504-5060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: MS DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: E. FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 45...65
                                                                                                                                                                                     APPLICANT: Loosmore, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
COMPUTER READABLE FORM:
                                                                                                                                TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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                               COUNTRY:
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                   M5G 1R7
                                                                   Toronto
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amino acid
GY: linear
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100.0%; s
tive 0;
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RESULT 10
US-08-782-832-15
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
                                     INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                 REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 36.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                      APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,334
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
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ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                   TELEPHONE: /13-850-0165
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 13-JAN
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 77027-9095
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STREET: 1177 West Loop South, 10th Floor
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COMPUTER: I
LENGTH:
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V: 425
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95.2%;
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US-08-817-906-21
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                                                                                                                                                                          RESULT 12
Sequence 14, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: UGAKA, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
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Matches
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Matches 20; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,906
FILING DATE: 08/04/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FOX, DAVID L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 36:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 103 amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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1301 McKinney, Suite 5100
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Pred. No. 1.1e-08;
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                                                                                                                                     NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 119
TYPE: PRT
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Matches 20; Conserv
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Best Local Similarity
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                                                                                                                                                                                                       FILE REFERENCE: Not Assigned CURRENT APPLICATION NUMBER: US/09/836,433 CURRENT FILING DATE: 2001-04-16
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                                                                                                                                                                                                                                                  APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
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APPLICANT: Udaka, Shigezo
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TYPE: PRT
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SOFTWARE: PatentIn version 3.0
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Local Similarity 95.2%;
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             1 GETFQVEVPGSQHIDSQKKAI 21
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RESULT 15 PCT-US99-30747-55

Sequence 55,

Application PC/TUS9930747

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GENERAL INFORMATION:

APPLICANT: Boyce Thompson Institute for Plant Research at Cor
ITITLE OF INVENTION: Grally Immunogenic Bacterial Enterotoxins Expressed In
ITITLE OF INVENTION: Transgenic Plants

FILE OF INVENTION: Expressed In

FILE OF INVENTION:
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Result
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Copyright (c) 1993 - 2002 Compugen
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US-09-791-537-38611
US-09-791-537-38639
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US-10-110-364-10
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US-10-110-364-17
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16, Appl
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US-10-110-364-22
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Best Local S
Matches 21
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TYPE: PRT
ORGANISM: Escherichia
FEATURE:
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27
89	89	89	89	89	89	92	92	95	95	95	101	101	101	101	101	101	101	101
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Sequence 1, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 123948,	Sequence 5, Appli	Sequence 129309,	Sequence 7, Appli	Sequence 42610, A	Sequence 33623, A	Sequence 8, Appli	Sequence 68591, A	Sequence 2, Appli	Sequence 130348,	Sequence 131854,	Sequence 15, Appl	Sequence 21, Appl	Sequence 19, Appl	Sequence 11, Appl	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-10-110-364-22
US-10-110-364-22
US-10-110-364-22
Sequence 22, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handparanta, Tapio
CURENT FILING DATE: 2000-10-05
FRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 05/158,561
PRIOR PILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 31
SOFTWARE: FASSED for Windows Version 4.0
SED ID NO 22
DESCRIPT: 103
LEBGTH: 103
CARANISM: Escherichia colli
PANTURE: PRT
DORATION: (1):-.(103)
COTHER INFORMATION: LITS variant from NCBI gene bank GI: 494265.
US-10-110-364-22
US-10-110-364-22
OUETY MATCH

OFTER INFORMATION: LITS variant from NCBI gene bank GI: 494265.
US-10-110-364-20
US-10-110-364-20
US-10-110-364-20
US-10-110-364-20
US-10-110-364-20
US-10-110-364-20
TITLE OF INVENTION: CHEMCAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO 00-04
CURRENT APPLICANT: Mandley, Harold H.
APPLICANT: Handley, Harold H.
APPLICANT: Handley Harold H.
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; ORGANISM: Escherichia coli
US-09-791-537-29489
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NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 223254.
US-10-110-364-20
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US-09-791-537-28360
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28360, Appl GENERAL INFORMATION:
                                                                      SEQ ID NO 29489
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Best Local Similarity
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Best Local :
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                     CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/1 PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05
                                   TYPE: PRT
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TYPE: PRT
                                                     ENGTH: 124
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Pred. No. 4.1e-10;
Mismatches 0;
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Pred. No. 4.1e-10;
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US-10-110-364-16
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SEQ ID NO 16
LENGTH: 124
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                                                       Matches
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Best Local Similarity
Matches 21; Conserv
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Best Local
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Best Local
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APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Danzer, JOSEPH
TITLE OF INVENTION: THREE DIMENSIONAL STRUC'
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                           NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1169505
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 124
TYPE: PRT
                                                                                                                                                                                                 FEATURE:
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Local Similarity 100.0%;
1 GETFQVEVPGSQHIDSQKKAI
                                                                      local Similarity
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                                                     Conservative
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                                                   Score 107; DB (
Pred. No. 4.1e-1
); Mismatches
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Pred. No. 4.1e-10;
); Mismatches 0;
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                                                                                        DB 6;
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66 GETFQVEVPGSQHIDSQKKAI 86

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Query Match
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, NAME/KEY: VARIANT
; LOCATION: (1)...(124)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 145833.
US-10-110-364-18
                                                                                                                         ; NAME/KEY: VARIANT; LOCATION: (1)...(124); COTHER INFORMATION: LTB variant from NCBI gene bank GI: 69630. US-10-110-364-23
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; Sequence 18, Application US/10110364
; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 23
LENGTH: 124
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
                                          Matches
                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHBMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A

CURRENT APPLICATION NUMBER: US/10/110,364

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: PCT/US00/27607

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 60/158,561

PRIOR APPLICATION NUMBER: 60/158,561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
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                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Escherichia coli
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                                          Conservative
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Pred. No.
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Pred. No. '
                                          Mismatches
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RESULT 11
US-09-791-537-38639
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US-09-791-537-38611
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US-09-791-537-19387
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 38611
LENCTH.
                         Sequence 38639, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Debe
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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APPLICANT: Bionomix, Inc.
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Josep
CURRENT APPLICATION NUMBER: US/09/791,537
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TYPE: PRT
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95.2%;
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95.2%;
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Pred. No.
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 74385
LENGTH: 103
TYPE: PAT
ORGANISM: pdb 1FGBD
US-09-791-537-74385
                                                                                                                                                                                                                              Sequence 10, Application US/10110364

GENERAL INFORMATION:

APPLICANT: Handley, Harold H.

APPLICANT: Hasparanta, Taplo

APPLICANT: Ewalt, Karla L.

TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS

FILE REFERENCE: ACTBIO.004A

CURRENT APPLICATION NUMBER: US/10/110,364

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: PCT/US00/27607

PRIOR FILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-10-05
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US-10-110-364-10
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US-09-791-537-74385
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; TYPE: PRT
; ORGANISM: pdb 1CHQD
US-09-791-537-38639
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Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                         SEQ ID NO 10
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                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                 LENGTH: 10
TYPE: PRT
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NAME/KEY: VARIANT LOCATION: (1)...(103)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511
                                                                           ORGANISM: Vibrio cholera
                                                             FEATURE:
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Pred. No. 3.4e-09;
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Pred. No. 3.4e-09;
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; NAME/KEY: VARIANT; LOCATION: (1)...(103)
; COTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235; OTHER INFORMATION: (Ogawa 41 R35D).
US-10-110-364-13
                                                                         ; ORGANISM: pdb 2CHBD
US-09-791-537-87980
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US-10-110-364-13
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Matches
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LENGTH: 103
TYPE: PRT
ORGANISM: Vibrio cholera
FEATURE:
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 Best Local Similarity Matches 20; Conserv
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Best Local Similarity
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APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: POT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                       APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                               TYPE: PRT
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                  94.48;
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Score 101; DB 5;
Pred. No. 3.5e-09;
0; Mismatches 1
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Pred. No. 3.4e-09;
0; Mismatches 1
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Pred. No. 3.4e-09;
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                                   Length 104;
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A;Residues: 1-17,'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A;Residues: 1-17,'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A;Cross-references: GB:S60731; NID:9408994; PIDN:AAC60441.1; PID:9408996
A;Cross-references: GB:S60731; NID:9408996
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A;Cross-references: GB:S60731; NID:940899898999999
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A;Title: Amino acid sequence of heat-labile enterotoxin A;Reference number: I53542; MUID:93252225
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J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between the
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A; Molecule type: DNA
A; Residues: 1-5, F; 7-17, C', 19-24, 'S', 26-27, 'E', 29-33, 'H', 35-63, 'K', 65-66, 'A', 68-122
A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831
A; Experimental source: plasmid ENT-R PCG86
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A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <YAM>
A; Residues: 1-27, 'E', 29-63; NID:g148335; PI
A; Cross-references: EMBL:M15363; NID:g148335; PI
R; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
A; Title: Nucleotide sequence comparison between
A; Reference number: I41194; MUID:85156481
A; Accession: I41194
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C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change
C;Accession: A01820; B26946; I41194; I41287; I67644; A61475
R;Dallas, W.S.; Falkow, S.
                                                                                                                                                                                                                                                                                                                            A;Reference number: I41287; MUID:87280041
A;Accession: I41287
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-124 Cojobori,
R; Yamamoto, T.; Gojobori, T.;
J. Bacteriol. 169, 1352-1357,
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GenCore version (c) 1993 - 2002

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A;Cross-references: GB:AE004224; GB:AE003852; NID:g9655952; A;Experimental source: serogroup O1; strain N16961; biotype R;Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J. Chinese Biochem. J. 9, 395-399, 1993
A;Title: Nucleotide sequence analysis of the gene encoding the property of the proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861
R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayron, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekkalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: H82196
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F;1-21/Domain: signal sequence *status predicted

F;22-124/Product: heat-labile enterotoxin chain E
F;30-107/Disulfide bonds: *status predicted
A;Residues: 1-20,'Q',22-31,'Q',33-38,'H',40-49,'G',51-67,'T',69-124
A;Experimental source: classical biotype strain 569B
R;Dams, E.; de Wolf, M.; Dierick, W.
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A;Accession: A61475
A;Molecule type: protein
A;Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124 <TSU>
A;Experimental source: strain 240-3
C;Complex: the heat-labile enterotoxin molecule contains one A chain and five or six B
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A: Posidues: 1-124 < LEW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholera enterotoxin, B chain precursor VC1456 [validated] - Vibrio cholerae
N;Alternate names: enterotoxin beta chain
C;Species: Vibrio cholerae
                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-124 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November {\bf A}_{\ell}{\bf Description}\colon Structure and arrangement of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1991 A; Description: Correction of the cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X76390; NID:g433856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-124 <L
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A; Accession: S39238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Lebens, M.; Holmgren,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X58786; NID:g48420; PIDN:CAA41593.1; PID:g48422
A;Exper1mental source: strain 2125
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A; Residues: 1-124 < DAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
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Pred. No. 5.9e-10;
; Mismatches 0;
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El Tor
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C; Keywords: enterotoxin; toxin
F;1-21/Domain: signal sequence #status predicted
F;22-124/Product: cholera enterotoxin chain B #si
F;30-107/Disulfide bonds: #status experimental
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A;Molecule type: protein
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
R;Takao, T.; Watanabe, H.; Shimonishi, Y.
Eur. J. Biochem. 146, 503-508, 1985
A;Title: Facile identification of protein sequences by mass spectrometry.
A;Reference number: A21910; MUID:85126976
A;Accession: A21910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124
R;Lai, C.Y
J. Biol. Chem. 252, 7249-7256, 1977
J. Fitle: Determination of the primary structure of cholera
A;Title: Determent: A88033; MUID:78005536
A;Reference number: A88033
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A;Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A;Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A;Cross-references: GB:X00171; NID:948347; PII
R;Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A;Title: Covalent structure of the beta chain
A;Reference number: A01819; MUID:78005537
A;Accession: A01819
                                                                                                                                                                                                                                                                                                                                                              \texttt{C;Complex:} the cholera enterotoxin molecule contains ciate noncovalently with the subunit B, an aggregate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124
A;Experimental source: biotype Inaba 569B
A;Note: Asn-65 was partially deaminated to Asp
C;Comment: The authors translated the codon TCA for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAT>
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAT>
A;Note: the difference at residue 70 may be due to deamidation during p:
R;Nakashima, Y., Naptorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
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A; Residues: 1-38, 'H', 40-67, 'T', 69-124 <DA2>
A; Cross-references: EMBL: X58785; NID: 948888; P
A; Cross-references: EMBL: X58785; NID: 948888; P
A; Cross-references: EMBL: X58785; NID: 948888; P
A; Title: B Subunit of Cholera toxin produced i
A; Title: B Subunit of Cholera toxin produced i
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R;Mekalanos, J.J.; Swartz, D.J.; Pearson,
Nature 306, 551-557, 1983
A;Reference number: A93320; MUID:84068199
A;Accession: A05130
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A;Title: Nucleotide sequence analysis of the
A;Reference number: S17665; MUID:91355224
A;Accession: S17666
                                                                                                                                                                                                                                                                          A;Description: involved in binding of the toxin to C;Superfamily: cholera enterotoxin beta chain
                                                                                                                                                                                                                                                                                                                                          C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
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A; Accession: PC1010
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                                                                                   Query Match
Best Local
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                                                                                                                                                                                             enterotoxin chain B #status predicted
21
                                                         0;
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Pred. No.
                                                            Mismatches
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Z
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Escherichia
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                                                            Indels
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66

86

GETFQVEVPGSQHIDSQKKAI

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C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04150
R;Schultz, T.F.; Quatrano, R.S.
Plant Mol. Biol. 34, 557-562, 1997
A;Tile: Characterization and expression of a rice RAD23 gene.
A;Reference number: 208695; MUID:97369378
A;Accession: T04150
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-992 <SCHP
A;Cross-references: EMBL:063530; NID:91488296; PIDN:AAB65841.1; PID:91488297
A;Experimental source: cv. Nipponbare
C;Gene: RAD23
C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Recession: A86457

A;Roccession: A86457

A;Residues: 1-255 (STO)
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
                                               C96580
hypothetical protein F15I1.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96580
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C; Genetics:
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    R;Theologis, Chin, C.W.;
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Best Local
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Best Local
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                                                                                                                                                                                                                                              GSTFQIEVDSAQKVADVKRII 30
    A.; Ecker, J.R.; Palm,
Chung, M.K.; Conn, L.;
                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conser
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                                                                                                                                                                                                                                                                                                                                                           43.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                              Score 47;
Pred. No.
C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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; Dewar, K.;
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C;Accession: C86400
C;Accession: C86400
C;Accession: C86400
C,Accession: C86400
A;Authors: Hughes, B.; Huizar, L.
CA, Lidy B16-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C,Ac; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia C,Ac; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                    Kinesin heavy chain-like protein - Arabidopsis thaliana N;Alternate names: protein MAA21.110 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #tex
                                                                                                                                                                                                                        RESULT 7
T49189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: C96580
                                              C; Accession: T49189
R; Rieger, M.; Mueller-Auer, S.; submitted to the Protein Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T17H3.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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C86400
A; Reference number: Z25018
A; Accession: T49189
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A; Map position:
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A; Residues: 1-574 <S'
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A; Residues: 1-91 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
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les 10; Conserv
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                                                Sequence
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                                                Zipp, M.; S
e Database,
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Pred. No. 3
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                                              Schaefer, M.;
, April 2000
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3.2;
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                                                                        Mewes,
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                                                                        H.W.; Rudd, S.;
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genome polyprotein - murine hepatitis virus (strain A59)
N;Alternate names: protein lb
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: murine hepatitis virus, MHV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: S15760; S08652
                                                                                         00
                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein 263 - Odontella sinensis chloroplast C;Species: chloroplast Odontella sinensis C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:x51939; NID:g58974; PID:g1334829 C;Superfamily: infectious bronchitis virus RNA-directed RNA C;Keywords: nucleotidyltransferase; RNA biosynthesis
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S15760
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A;Residues: 1-439 <RIE>
A;Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.110
                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-263 <KOW>
                                                                                                                                                                                                                                                           A; Reference number: S78238
A; Accession: S78364
                                                                                                                                                                                                                                                                                     R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U. Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella
                                                                                                                        A; Genome: chloroplast
                                                                                                                                        A; Gene: ycf43
                                                                                                                                                                         A; Note: the nucleotide sequence
                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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A;Accession: S15760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frameshifting mechanism
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A; Introns: 39/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: The primary structure and
                                                                                     Superfamily: conserved:
Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Best I
                    Matches
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                      Similarity
8; Conserv
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9; Conser
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8; Conserv
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                      Conservative
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                                                                                                                                                                       EMBL: 267753; NID:g1185127; PIDN: CAA91737.1; PID:g1185254 ide sequence was submitted to the EMBL Data Library, Nove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97/3; 138/3; 147/2;
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                                  41.1%;
40.0%;
                                                                                                       hypothetical protein HI0188
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                                  Score 44; DB
Pred. No. 21;
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Pred. No. 1.76
2; Mismatches
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Pred. No.
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1.7e+02;
6;
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                    6;
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                   0;
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genome polyprotein 1b - murine hepatitis virus (strain N;Alternate names: 1b protein N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48) C;Species: murine hepatitis virus, MHV C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #tex C;Accession: B36815
                                                                                                                                                                                                                                                                                                       A; Gene: NCSP:B208.220
A; Map position: 6
A; Introns: 138/1
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                                                                                                        VEIHJH
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A; Accession: T49574
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8; Conserv
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C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision
C;Accession: T49574
                                                                                                                                                                                                                                                                                                                                R;Schulte, U.; Aign, V.; Hoheisel, J.; Brand submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: X
A; Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C; Superfamily: Caenorhabditis elegans hypo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C40H5.3 - Ca
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                      probable carnitine acetyl transferase FacC [imported] - Neurospora
N;Alternate names: protein B208.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A; Reference number: Z19189
                                                                                                                                                                                                                             A;Cross-references: EMBL:AL355930; GSPDB:GN00116; NCSP:B208.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z81482; PIDN:CAB03954.2; GSPDB:GN00028; CESP:C40H5.3
A;Experimental source: clone C40H5
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QTFWADAPGDAKIDALRKA
                               ETFQVEVPGSQHIDSQKKA
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                                                                 Similarity 42.3
8; Conservative
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                                                                 Score 44; DB Pred. No. 73; 4; Mismatches
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                                                                                                    Length 864;
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31-Dec-1992 #text_change

11-Jun-1999

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R;Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd submitted to GenBank, February 1991
A;Description: The complete sequence (22 kilobases) of murine coronavirus gene 1 encodin A;Reference number: A36815
A;Accession: B36815
A;Molecule type: genomic RNA
A;Residues: 1-2731 <-LEE>
A;Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853
R;Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd Virology 180, 567-582, 1991
A;Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the A;Reference number: A38547; MUID:91111976
A;Rote: neither nuclectide nor complete amino acid sequence is given C;Comment: This protein may be translated as a la-1b polyprotein by a ribosomal frameshi C;Genetics:
A;Gene: 1b
C;Superfamily: infectious bronchitis virus RNA-directed RNA polymerase C;Keywords: glycoprotein; nuclectidyltransferase; RNA blosynthesis
F;269,304,785,1184,1287,1524,1842,2196,2575,2630,2645,2665/Binding site: carbohydrate (A)
                                        RESULT 14
UQDOR
UDGOR
UDGOR
UDGOR
N;Alternate names: ubiquitin fusion protein
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 31-Dec-1990 *sequence_revision 31-Dec-1990 *text_change :
C;Accession: S00357; A25863
C;Accession: S00357; A25863
R;Mueller-Taubenberger, A.; Westphal, M.; Jaeger, E.; Noegel, A.
FFRS Lett. 229, 273-278, 1988
FFRS Lett. 229, 273-278, acquence of a Dictyostelium ubiquitin with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: (C;Genetics: A;Gene: At2g31880 A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable receptor-like protein kinase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84726 C;Accession: C84726 R;Lin, X; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Jeuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence and analysis of chromosome
A;Reference number: A84420; MUID:20083487
A;Accession: C84726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-641 <STO>
A;Title: Complete cDNA sequence of a Dictyostelium A;Reference number: S00357; MUID:88152253 A;Accession: S00357 A;Molecule type: mRNA
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Best Local
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9; Conserv
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A;Cross-references: GB:M23750; GB:J02858; NID:g167940; C;Superfamily: ubiquitin / rat ribosomal protein S27a; C;Keywords: protein biosynthesis; protein degradation; E;1-76/product: ubiquitin #status predicted <MATI> F;1-76/pomain: ubiquitin homology <UBH>
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A;Cross-references: EMML:X07210; NID:g7381; PIDN:CAA30183.1;
A;Experimental source: strain AX2-214
C;Genetics:
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DPOL_THEST
PMS2_HUMAN
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HEFA_AERPE
HS74_CAEEL
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p13811 escherichia
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p16342 murine coro
p49538 odontella s
o14896 homo sapien
p97431 mus musculu
p29982 murine coro
p18618 dictyosteli
p10039 gallus gall
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p28777 saccharomyc
p80404 homo sapien
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p30317 thermococcu
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p13117 neurospora
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p20163 caenorhabdi
Q924t9 rattus norv
Q10005 caenorhabdi
Q24857 entamoeba h
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Mol. Microbiol. 15:1165-1167(1995).

"IF FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."

"I- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS."
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[7]
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R; B26946; QLECEB.

R; B17A; 31 JAN-94.

R; LITB; 31 JAN-94.

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RITI; 31 JAN-94.

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P13811;
01-JAN-1990
                                                                                                                                                              activity.";
J. Biol. Chem. 274:8764-8769(1999).
-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                        comparison of correct amino acid sequences enterotoxins of Escherichia coli and Vibrio Mol. Microbiol. 15:1165-1167(1995).
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STRAIN-ISOLATE H74-114;
MEDLINE-85156481; PubMe
                                                                                      the
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or send
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Submitted (OCT-1996) to
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Inoue T., Tsuji T., Koto M., Imamura S., Miyama
"Amino acid sequence of heat-labile enterotoxin
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MEDLINE=83114628; PubMed=6759877;
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Leong J., Vinal A.C., Dallas W.S.;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile
cistrons from Escherichia coli of human and porcine
Infect. Immun. 48:73-77(1985).
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Bacteria; Proteobacteria;
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s requires a license agreement (S an email to license@isb-sib.ch).
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21-UUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence up
16-CCT-2001 (Rel. 40, Last annotation
                                                                                                                    SEQUENCE FROM N.A. STRAIN-EL TOR 2125; Dams E., de Wolf M., I Submitted (MAY-1991)
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VARIANT
VARIANT
                                                                                                                                                                          de Wilde M.;
"Cholera toxin genes:
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STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
MEDLINE-84068199; PubMed-6646234;
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PDB; 1LTR; 23-MAR-99.
InterPro; IPR001835; Enterotoxin_B.
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MEDLINE=84061784; PubMed=6315707;
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 Submitted
                                                           cholerae 0139
                                                                                   STRAIN=4260B / SEROTYPE 0139;
MEDLINE=94237453; PubMed=8181723;
                                                                                                                                                       Nature 306:551-557(1983).
[3]
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"Nucleotide sequence analysis of the
cholerae enterotoxin ":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterotoxin; Signal;
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STRAIN=1854 / 0139-BENGAL;
        Honda T.
                Yamamoto K.,
                                                                    Structure
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CAA58800.1;
                Do V.G.R.F.,
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Merritt E.A., Sarfaty S., Jobling M.G., Charlet Hirst T.R., Hol W.G.J.;

"Structural studies of receptor binding by cholera toxin mutant "Structural studies of receptor binding by cholera toxin mutant Protein Sci. 6:1516-1528 (1997).

-I- FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED BINDING TO CELL MEMBRANES.

-I- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA (FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAI DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE
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SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton
Heidelberg J.F., Hickey E.K., Peterson J.D.
                       EMBL;
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P. McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.
                                                                                                                         entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=OGAWA 41 / CLASSICAL BIOTYPE; MEDLINE=97376625; PubMed=9232653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang R.G., Westbrook M.L., Westbrook E.M., Maulik P.R., Reed R.A., Shipley G.G.; "The 2.4 A crystal structure of cholera tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=95387394; PubMed=7658472;
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Kurosky A., Markel D.E., Peterson J.W.
"Covalent structure of the beta chain
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MEDLINE-94272319; PubMed-8003954;
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                      X00171; CAA24996.1; -...; K01170; AAA27573.1; -...; D30053; BAA06291.1; -...; X58786; CAA41593.1; -...; X76390; CAA53973.1; -...; X76391; CAA53976.1; -...; X76391; CAA53976.1; -...;
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A05130; S14624;

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HELIX
                      MEDLINE=90245573; PubMed=
Bredenbeek P.J., Pachuk C
Weiss S.R., Spaan W.J.M.;
                                                 Murine coronavirus MHV (strain viruses; ssRNA positive-strand Coronavirus. NCBI_TaxID=11142;
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"The primary structure and expression of the second open reading frame of the polymerase gene of the coronavirus MHV-A59; a highly conserved polymerase is expressed by an efficient ribosomal frameshifting mechanism.";
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30-MAY-2000
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23-DEC-96.
01-APR-97.
01-AUG-96.
15-OCT-97.
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12-AUG-98.
08-MAR-96.
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d RNA polym
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merase (EC 2.7.7.48) (
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-1- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES
A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESS
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
SUBGENOMIC MRNAS AND PROGENY VIRION RNA.

SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                         Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae; Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella. NCBI_TaxID=2839;
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                                                                                                                                                                     Plant Mol. Biol. Rep. 13:336-342(1995).
                                                                                                                                                                                            Odontella sinensis
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                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane
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S15760;
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9; Conserv
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69;
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PRINTS; PR00267; INTERNREGECT.
PRODOM; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
PROSITE; PS00601; IRF; 1.
Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
DNA_BIND 9 131 TRYPTOPHAN PENTAD REPEAT.
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TRANSMEM 1
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SEQUENCE
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                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                            Grossman A., Mittrucker
Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                           Grafham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Interferon regulatory factor 6 (IRF-6).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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QVKFPGPEHITNEKQKL
                      QVEVPGSQHIDSQKKAI 21
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8; Conserv
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Primates;
                                                       41.18;
41.28;
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Pred. No.
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5; Mismatches
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IRF6_MOUSE
P97431;
  MEDILINE-91111976; PubMed-1846489;
Lee H.-J., Shieh C.-K., Gorbalenya A.E.,
Tuler J., Bagdzhardzhyan A., Lai M.M.C.;
"The complete sequence (22 kilobases) of
encoding the putative proteases and RNA periology 180:567-582(1991).
                                                                                                                                                                                                                                                               Murine coronavirus MHV (strain JHM).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRPB_CVI
P29982;
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HSSP; P23906; 2IRF.
MGD; MGI:1859211; Irf6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C; TISSUE-Colon;
Grossman A., Mittrucker H.W., Antonio L., Mak
Submitted (CCT-1996) to the EMBL/GenBank/DBN
Submitted (CCT-1996) to the EMBL/GenBank/DBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; DNA-binding; Nuclear DNA_BIND 9 111 TRYPTOPHAN PENTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Pfam; PF00605; IRF; 1
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    -!- SIMILARITY: BELONGS TO THE IRF FAMILY.

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     POLYMERASE OF CORONAVIRUSES
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                                                          coronavirus
ase.";
                                                                                                                                     Ε.Υ.,
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Best Local
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01-AUG-1988
01-AUG-1988
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Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
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NP_BIND
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DOMAIN
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                                                                                                                                                                                                                                                                "Molecular organization of developmentally regulated Dictyostelium discoideum ubiquitin cDNAs."; Biochemistry 28:5226-5231(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88152253; Puk
Mueller-Taubenberger
    Westphal
                             STRAIN-AX2;
                                                                                              ubiquitin genes.
Mol. Cell. Biol.
                                                                                                                                                                      Giorda R.,
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-89352609; PubMed-2548604;
Ohmachi T., Giorda R., Shaw D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBIQ_DICDI
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                                                     SEQUENCE OF
                                                                                                                                         Giorda R., Ennis H.L.;
                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=87257921;
                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminal tail and antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete cDNA sequence of a Dict
terminal tail and identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECES FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA, SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RNA)(N)
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9; Conser
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    Mueller-Taubenberg
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ger A., Westphal M.,
                                                                                                                                            developmentally regulated Dictyostelium discoideum
                                                                                                                                                                                            PubMed=3037345;
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Dictyosteliida;
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Pred. No. 1e+(
0; Mismatches
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CYS/HIS-RICH.
HELICASE.
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    Α.,
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99463066B1776970
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    Noegel
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le+02;
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Best Local S
Matches 9
CHICK
TENA_CHICK STANDARD; PRT; TUNG_TENA_CHICK
P10039; P13132; O73584; O73585;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation) (Cytote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
VARIANT
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EMBL; X07210; CAA30183.1; ALT_TERM.
EMBL; M1966; AAA33261.1; ALT_TERM.
EMBL; M19491; AAA33269.1; ALT_TERM.
EMBL; M19492; AAA33270.1; ALT_TERM.
EMBL; M19492; AAA33270.1; ALT_TERM.
EMBL; M23748; AAA33263.1; ALT_TERM.
EMBL; M23750; AAA33263.1; ALT_TERM.
EMBL; M23750; AAA33264.1; ALT_TERM.
EMBL; M23751; AAA33265.1; ALT_TERM.
EMBL; M23752; AAA33266.1; ALT_TERM.
EMBL; M23753; AAA33266.1; ALT_TERM.
EMBL; M23754; AAA33266.1; ALT_TERM.
EMBL; M23754; AAA33268.1; ALT_TERM.
EMBL; M23754; AAA33268.1; ALT_TERM.
EMBL; X04702; CAA28408.1; ALT_TERM.
EMBL; X04702; CAA28408.1; ALT_TERM.
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PIR; B37806; E
PIR; A34080; B
PIR; B34080; B
PIR; C34080; C
PIR; D34080; D
HSSP; P02248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DictyDb; DD05001; ubqA.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Transcript regulation and carboxyterminal extension Dictyostelium discoideum.", FEBS Lett. 209:92-96(1986).
-i- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00348; UBIQUITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires
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MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES
CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S00357;
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GKTITLEVEGSDNIENVKAKI
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                                                                                                                                                           h 40.2%;
Similarity 42.9%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00299;
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                                                                                                                                                                                                                                                                                                                           76 AA;
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UQDOR7.
A27806.
B27806.
A34080.
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UBIQUITIN_2; 1.
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5; Mismatches
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CONJUGATION TO ACCEPTOR PROTEINS K -> N (IN SOME CLONES REPEATS).
6427383968EA8884 CRC64;
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lon) (Cytotactin) (Neuronectin)
(Glioma-associated-extracellular

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RT GIOWTH FACTOR-LIKE repeats and segments of fibronectin and refringen.";

RT fibrinogen.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:2186-2190(1988).

C. -!- FUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPEARS TO INHEBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWTH COMPANY OF PETITHELIAL TUMORS. IS A LIGAND FOR INTEGRINS ALPHA-8/BETA-1, ALPHA-V/BETA-3 AND ALPHA-V/BETA-6.

C. -!- SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COLLED-COIL REGION AND MAY BE STABLIZED BY DISULFIDE RINGS AT COMPANY THE CENTRAL GLOBULE.

C. -!- SUBCLULAR LOCATION: EXTRACHIONS MAY BE DISULFIDE LINKED WITHIN THE CENTRAL GLOBULE.

C. -!- SUBCELLULAR LOCATION: EXTRACEILLAR MAY BE DISULFIDE LINKED COMPANTIVE PRODUCTS: 3 ISOFORMS; 230 KDA (SHOWN HERE), 200 KDA CAND 190 KDA; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ARE PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.

C. -!- INDUCTION: BY TGF-BETA.

C. -!- SIMILARITY: CONTAINS 13.5 EGF-LIKE DOMAINS.

C. -!- SIMILARITY: CONTAINS 11 FIBRONECTIN TYPE III-LIKE DOMAINS.

C. -!- SIMILARITY: CONTAINS 13 FIBRONECTIN TYPE III-LIKE DOMAINS.
              EMBL; M23
EMBL; X08
EMBL; J03
EMBL; J03
EMBL; M20
PIR; A319
PIR; B333
PIR; B333
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Edelman
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Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE=90030407;
Spring J., Beck K.
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"Two contrary functions
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                                           A33379; E
B33379; E
C33379; C
S01292; S
P24821;
                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions how non-profit institutions as long as its content is in
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A31930;
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,; X08031; CAB40811.1;
,; X08030; CAA30824.1;
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EGF-LIKE 1.
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MEDLINE=99432178; PubMed=10500122;

Takeuchi T., Shuman M.A., Craik C.S.;

Takeverse biochemistry: Use of macromolecular protease inhibitors idesect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";

Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99303581; PubMed-10373424;

Lin C.Y., Anders J., Johnson M., Sang Q.A.,

"Molecular cloning of cDNA for matriptase,

protease with trypsin-like activity.";

J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                STA14_HUMAN STANDARD; PRT; 855 AA.

99Y5Y6; 09H3S0; Q9HCA3; Q9BS01; Q9HB36;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15
(Tumor associated differentially-expressed gene-15 protein).

ST14 OR PRSS14 OR SNC19 OR TADG15.
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"Molecular cloning
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Pfam; PF00431; CUB; 2. 4. Pfam; PF00057; Idl_recpt_a; 4. Pfam; PF00089; Trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN. PRINTS; PR00726; LDLRECEPTOR. SMART; SM00142; CUB; 2. SMART; SM00192; LDLa; 3. SMART; SM001020; Tryp_SPC; 1. SMART; SM001020; Tryp_SPC; 1.
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EMBL; AF133086; AAF00109.1;
EMBL; AB030036; BAB20376.1;
EMBL; AF057145; AAG15395.1;
EMBL; BC005826; AAG15826.1;
EMBL; AF283256; AAG13949.1;
HSSP; P00763; 1DPO.
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MEDLINE-99303582; PubMed-10373425;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
Purification and characterization of a complex containing matriptase and a kunitz-type serine protease inhibitor from human milk.";
J. Biol. Chem. 274:18237-18242 (1999).

-i- FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PRODOSED TO PLAY A ROLE IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic analysis of a n
Submitted (JUN-2000) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUOR LYS AS THE PI SITE.
SUBCELLULAR LOCATION: Type II membrane protein
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DON
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Enteropean Bioinformatics Institute. There are no restruction by non-profit institutions as long as its content
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i (JUL-1999) to
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d; Tryp_SPc;

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AROC_YEAST STANDARD; PRT; 3/v....
P28777;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                      SEQUENCE FROM STRAIN-S288C / FY1769;
STRAIN-S288C / FY1769;
MEDLINE-97197983; PubMed-9046099;
Voet M., Defoor E., Verhasselt P., Riles L., Foet M., Defoor E., Verhasselt P., Foet M., 
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 50.6; Conservative
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N-LINKED (GLCNAC. 
FEA -> GIR (IN REF. 3) 
R -> S (IN REF. 4).
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Pred.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CUB 1.
CUB 2.
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e synthase, of Saccharomyces
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siae reveals ARO
frames.";
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(BY SIMILARITY).
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the left arm
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABT_HUMAN STANDARD; PRT; DUU AA.
P80404;
P80404;
01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-aminobutyrate aminotransferase, mitochondrial precursor
(EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT).
VARIANT LYS-220.

MEDLINE-99356116; PubMed-10407778;

Medline-Fauwe L.K., Tobin A.J., De Meirleir L., Jaeken

Myhan W.L., Gibson K.M.;

4-aminobutyrate aminotransferase (GABA-transaminase)

J. Inherit. Metab. Dis. 22:414-427(1999).

-1- CATALYTIC ACTIVITY: 4-aminobutanoate + 2-oxoglutan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01264; Chorismate_synt; 1.
ProDom; PD002941; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid biosynthesis.
SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                          MEDLINE-95154329; PubMed-7851425; de Biase D., Barra D., Simmaco M., John R.A., "Primary structure and tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                            "Screening and sequence determination of brain 4-aminobutyrate aminotransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osei Y.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95237607; PubMed=7721088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 368-465 FROM
                                                                                                                                                                                                                                                                                                                                                                                        Gene 155:185-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD; S0003116; ARO2.
InterPro; IPR000453; Chorismate_synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION: BY AMINO ACID STARVATION. SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; X60190; CAA42745.1; -.; X99960; CAA68214.1; -.; Z72670; CAA96860.1; -. S17246; S17246.
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Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
                                                                                                                                                                                             227:476-480(1995).
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           AND
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human
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4-aminobutyrate
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Matches
                                                                                                                                                                                                                                                                                             P28369; P77246;
01-DEC-1992 (Rel. 24, C
01-DEC-1992 (Rel. 24, L
16-OCT-2001 (Rel. 40, L
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BINDING
VARIANT
                               SEQUENCE FROM N.A STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        Peptide chain release
PRFH OR B0236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - - - -
      MEDLINE-90330577;
                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                             RFH_ECOLI
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HSSP; P80147; 1GTX.
                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                        Escherichia
                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000954; Aminotran_3.
Pfam; PF00202; aminotran_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 137150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
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DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT PHENOTYPE INCLUDES PSYCHOMOTOR RETAKDATION, HYPO HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                semialdehyde + L-glutamate.
COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KIDNEY >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMINOTRANSFERASES
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SIMILARITY: BELONGS TO CLASS-III OF
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   PubMed=1695895;
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D -> H (IN REF. 2)
V -> L (IN REF. 2)
E -> G (IN REF. 2)
K -> Q (IN REF. 2)
K -> Q (IN REF. 2)
S -> A (IN REF. 2)
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4-AMINOBUTYRATE AMINOTRAI
PYRIDOXAL PHOSPHATE.
R -> K (IN GABA-AT DEFIC.
R EDUCTION IN ACTIVITY).
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Pred. No. 41;
4; Mismatches
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhaw G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Yanamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihar Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K "Systematic sequencing of the Escherichia coli genome: analysis 4.0 - 6.0 min (189,987 - 281,416bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                            EMBL;
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-i- FUNCTION: COULD BE PROTEIN FACTOR INVOLVED
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Lashkari D., Lew H.,
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genes.";
J. Bacteriol. 172:4641-4651(19)
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"Peptidase D gene (pepD) of Escherichia coli K-12: nucleotide
                                                                      SEQUENCE
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InterPro; IPR000352; Pe
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SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
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  ETFQVEVPGSQHIDSQKKAI
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AE000132; AAC73340.1; -
D8536; BAA7905.1; -
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9D2EBD9AF7A04831 CRC64;
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, Mizobuchi K.;
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YP68_CAEEL
Search completed: October 24, 2002, 15:21:04 Job time: 9.26229 secs
                                                                                                                                   Query Match 38.3%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YP68_CAEEL STANDARD: PRT; 313 AA.
Q09217;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 37.0 kDa protein B0495.8 in chromosome II.
B0495.8.
                                                                                                                                                                                                    EMBL; U21317; AAA62527.1; -. WormPep; B0495.8; CE01766. Hypothetical protein. SEQUENCE 313 AA; 36977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         Kirsten J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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11 QLMGSQHVDNKEK 23
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Pred. No.
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Q39v32 escherichia
Q94m01 vibrio phag
Q9r646 vibrio chol
Q99987 homo sapien
Q91jb0 arabidopsis
Q90e815 arabidopsis
Q90e875 arabidopsis
Q91gm2 oryza sativ
Q40742 oryza sativ
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Q9syf4 arabidopsis
Q9syc9 arabidopsis
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Q9syc9 arabidopsis
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ALIGNMENTS

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Q94e00 oryza sativ		Q947w6 oryza sativ	Q965w6 caenorhabdi	-			pseudo	gallus	Q90995 gallus gall	rhizok	Q918i7 hepatitis b		Q9sn44 arabidopsis	Q9nf90 leishmania		Q9skb2 arabidopsis	Q9p606 neurospora	Q91vd0 mus musculu	Q9n136 ovis aries	Q9u3m9 caenorhabdi	_	049876 lupinus alb	O22511 vitis vinif	murin	039226 murine hepa	murine	Q9j3f2 murine hepa	Q9ly67 arabidopsis

RESULT 1 Q57193 Q57193 PRELIMINARY; C7193; Q57193; Q57199; Q571996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1996 (TrEMBLrel. 17, Last annotation update) Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update) CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB). ProDom; Signal. Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases. EMBL; X58785; CAA41591.1; -. EMBL; U25679; AAC34728.1; -. EMBL; A00931; CAA00098.1; -. HSSP; P01556; 2CHB. STRAIN=CLASSICAL STRAIN 569B; MEDLINE=91355224; PubMed=188840; Dams E., De Wolf M., Dierick W.; "Nucleotide sequence analysis of the CT operon classical strain 569B."; Dierichte Beichte Auf 1000:130-141/1001; InterPro; IPR001835; Enterotoxin_B. Pfam; PF01376; Enterotoxin_B; 1. PRINTS; PR00772; ENTEROTOXINB. STRAIN=CLASSICAL BIOTYPE 569B; Shi C., Cao C., Zhang J., Ma Q.; Chin. Biochem. J. 9:395-399(1993). SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Bacteria; Proteobacteria; NCBI_TaxID=666; Vibrio cholerae Xu L.; STRAIN-CLASSICAL BIOTYPE 569B; Biochim. Biophys. Acta 1090:139-141(1991). PD012805; Enterotoxin_B; gamma subdivision; Vibrionaceae; Vibrio. of the Vibrio cholerae

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                                                 "Comparison of cholera toxin strains 854 (0139-bengal) and submitted (APR-1994) to the EEMBL; D30052; BAA06289.1; HSSP; P01556; 2CHB.
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01.NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
CHOLERA TOXIN PRECURSOR.
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ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae
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EMBL; AF175708; AAD51360.1; -.
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Honda T.;
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Pfam; PF01376; Enterotoxin_B; 1.
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Shin H.J., Park Y.C.,
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20; Conser
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PD012805; Enterotoxin_B; 1.
E 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
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CHOLERA TOXIN B PROTEIN (CTB).
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Pred. No.
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Pred. No. 3.
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Bhattacharyyaa T., Nandy R.K.,
"The entire core region of the
environmental strain of V. chol
                                                                                   Vibrio phage CTX.
Viruses; ssDNA viruses;
NCBI_TaxID=141904;
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01-DEC-2001
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MEDLINE-95091056; PubMed-7998417;
Tamura S., Asanuma H., Tomita T., K.
Hattori N., Watanabe K., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Escherichia.
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EMBL; AB011677; BAA25726.1;
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Q1-JAN-1998
Q1-DEC-2001
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Q9R646;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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pfam; pF01376; Enterotoxin_B; 1.
prINTS; pR00772; ENTEROTOXINB.
proDom; pD012805; Enterotoxin_B; 1.
seQUENCE 103 AA; 11645 MW; 992A05C077F2E70E CRC64;
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Bacteria; Proteobacteria;
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EMBL; AF414369; AAL09
                   Genomics 45:327-331(1997).
-!- SIMILARITY: BELONGS TO EMBL; AB000450; BAA19109.1; HSSP; Q06486; 1CKI.
                                                                                                           MEDLINE-98008921; PubMed=9344656;
Nezu J., Oku A., Jones M.H., Shimane M.;
"Identification of two novel human putative serine/threonine VRK1 and VR K2, with structural similarity to Vaccinia virus
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                                                        OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                        KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio
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                                                                                                               B1R
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RESULT Q9C815
ID Q9C815
ID TO 01
DT 01
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LJB0;
01-OCT-2000 (TrE
01-OCT-2000 (TrE
01-DEC-2001 (TrE
EMB|CAB77996.1.
                                                                                                                                                                                                                                                                                                            O9C815; PRELIMINARY; PRT; 255 AA.
O9C815; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence up
O1-JUN-2001 (TrEMBLE). 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; 2.

PROSITE; PS50011; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Serine/threonine-protein kinase; T1

SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4
SEQUENCE FROM N.A. STRAIN-CV. COLUMB: MEDLINE-21016719;
                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP000606; BAB01195.1;
SEQUENCE 552 AA; 63036 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis
Sequence features of
TAC and BAC clones.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9LJB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002290;
Pfam; PF00069; pkinas
                                                                                                                                                                                                                                                                        F10C21
                                                                                                                                                                                                                                                                                             PEPTIDE CHAIN RELEASE FACTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 GQSINVHTPNSQKVDSQKAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GETFQVEVPGSQHIDSQKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVEIPASMEIDEETKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
10; Conserv
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OCT-1999)
                              COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, CTEMBLrel. 15, CTEMBLrel. 19, CTEMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
      PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
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se; 2.
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e regions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.9
2; Mismatches
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
                                                                                                                                                                                                                                                                                                PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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1.2;
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?.9;
                                                                                                                                                    Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabata
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                                                                                                                                                                                Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Liv.

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Luros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
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RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lim B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9C875

Q9C875;

O1-JUN-2001 (TrEMBLrel. 17, Created)
T 01-JUN-2001 (TrEMBLrel. 17, Last seque)
JT 01-JUN-2001 (TrEMBLrel. 17, Last annot
"VPOTHETICAL 27.6 KDA PROTEIN.
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Best Local
thaliana.";

Nature 408:816-820(2000).

EMBL; ACC27035; AAG51290.1;

InterPro; IPR000352; Pep_re

Pfam; PF00472; RF-1; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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EMBL; AC05130; AA651209 1; -.
InterPro; IPR000352; Pep_rel_factor_I.
Pfam; PF00472; RF-1; 1.
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NCBI_TaxID=3702;
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      Pep_rel_factor_I
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Pred. No.
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Araujo R., Bowman C.L., Brooks
hen H., Cheuk R.F., Chin C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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annotation update)
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3.9;
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edons; core eudicots; Rosid
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RESULT 12
Q40742
ID Q4074
AC Q4074
AC Q4074
AC 01-NO
DT 01-NO
DT 01-SE
DE OSRAD
OS OIYZA
OC EUKAR
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Matches
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Best Local
                                                                             01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                              Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                            Q40742;
Q40742;
                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0433E09.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza,
NCBI_TaxID=4530;
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01-OCT-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
                                                                     OSRAD23
                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2000) to the EMBL; AP002521; BAA96762.1; EMBL; AP002539; BAB08201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      "Oryza sativa nipponbare(GA3) genomic clone:P0041E11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTS AU056822(S20908).
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                                                            6 (TrEMBLrel. 01, 6 (TrEMBLrel. 01, 1) (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aı protein.
257 AA; 2
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                                                                                                                     PRELIMINARY;
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45.0%;
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52.6%;
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                                                                             Last sequence update)
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Pred. No.
                                       Liliopsida;
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SEQUENCE

NCBI_TaxID=4530;

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Q9NKD5

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AC Q9

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InterPro; IPRO00626; Ubiquitin.
Pfam; PF00627; UBA; 2.
Pfam; PF00240; ubiquitin; 1.
SMART; SM00165; UBA; 2.
SMART; SM00165; UBQ; 1.
PROSITE; PS50053; UBIQUITIN_2; 1
SEQUENCE 392 AA; 41754 MW; B
                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-Y, CN BW SP;

Celniker S.E., Abbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Celniker S.E., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.

Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.

Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearrey L., Kim E., Lee B.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

Mixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Zieran L.L., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AE003408; AAF44847.1;

THERES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NKD5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
BG:DS01514.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshre Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc.

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                             Hypothetical protein.
SEQUENCE 395 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Y, CN BW SP;
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                                                                                                                                                                                            FlyBase; FBgn0028907; BG:DS01514.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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U63530; AAB65841.1;
P54725; 1DV0.
                                            Similarity
9; Conserv
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9; Conser
                                            Conservative
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                                                                                                                                             43561 MW;
                                                                    43.9%;
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                                            2;
                                                                 Score 47;
Pred. No.
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Pred. No.
                                                                                                                                             AE4F1CC4ADD3DA73 CRC64;
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                                               Mismatches
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                                                                      DB
14;
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                                                                                           Length 395;
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                                               Indels
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QVEVPGSQHIDSQKKA

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RESULT
QSYF4
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Best Local
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01-MAY-2000
01-DEC-2001
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                                                                                                                         STRAIN-CV. COLUMBIA;

Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.

Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano

Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks

Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,

Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M

Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9SXC9; PRELIMINARY; PRT; 574 AA.
O9SXC9; U1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat)
T17H3.2 PROTEIN (ATIG27520/T17H3_2).
T17H3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hanser Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker N. Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC F1511 sequence."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
  Bowser L.,
Ishida J.,
                    Cheuk R., Chen H., Kim C.J.,
Bowser L., Carninci P., Dale
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta;, eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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InterPro; IPR000626; Ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R.,
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  Jiang P.X.,
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Last sequence up
Last annotation
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Koesema E., Meye
J.M., Goldsmith
T., Kamiya A., F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ced. No. 3.8;
Mismatches
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                            Meyers M.C.,
nith A.D., Ha
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     Karlin-Neumann
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                               Result
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   Score
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1: /cgn2_6/ptodata/1/paa/US

2: /cgn2_6/ptodata/1/paa/US

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13: /cgn2_6/ptodata/1/paa/US
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Cgn2_6/ptodata/1/paa/US087_COMB.pep:
Cgn2_6/ptodata/1/paa/US088_COMB.pep:
Cgn2_6/ptodata/1/paa/US089_COMB.pep:
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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52.114 Million cell updates/sec
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e 4,	Sequence 4, Appli	3, 1	ω	1, A	e 328,	318, Ap	15(7, 2	e 35,		32551,	32459,		29272,	5651,	Sequence 2967, Ap	154	5	e 6,	3, Ap	22,	18,	15,		2	57,	e 55,	57, App	55, 2	22,	20,	14,	21,	e 15	2,	26,	Sequence 26, Appl

ALIGNMENTS

RESULT 1 US-09-786-648-2

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; TYPE: PRT; ORGANISM: E. COL1; FEATURE: 51...57; LOCATION: 51...57; OTHER INFORMATION: 1; OTHER INFORMATION: 1; OTHER INFORMATION: b; OTHER INFORMATION: d; OTHER INFORMATION: 
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GENERAL INFORMATION:

APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 2
                                                                          Query Match
Best Local
                  Matches
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            Local Similarity hes 7; Conserv
                  Conservative
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Score 39; DB zı;
Pred. No. 3.2e+06;
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Sequence 1
Sequence 1
Sequence 4 4443

Sequence

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US-08-732-371-1
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                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,371
FILING DATE: 09-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
TI 100510
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APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymon
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SEQ ID NO 3
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APPLICATION UNMBER: IL 109519
APPLICATION UNMBER: 11 109519
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MIRELM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hirst, Timothy Raymond TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine TITLE OF INVENTION: Adjuvants FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 50...61
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVPGSQH 7
|||||||
2 EVPGSQH 8
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARKS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SELA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIRELMAN, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACCINES FOR ORAL IMMUNIZATION AGAINST INFECTING AGENTS
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                                          MIRELMAN=3
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Query Match
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                                                                                                           US-08-732-371A-1
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The 7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: IL 10 FILING DATE: 03-MAY-1994 AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARKS, RO APPLICANT: SELA, M10 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                          TELEPHONE: 202-737-3528
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/732,371A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                         NAME: YUN, Allen C.
2 EVPGSQH
                          1 EVPGSQH 7
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                                                                                                                                      amino acid
GY: linear
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419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                    Conservative
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OR SEQ ID NO:
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Pred. No.
                                                                  Score 39;
Pred. No.
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RESULT 5 US-09-786-648-4

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; FEATURE:
; LOCATION: 45...65
; OTHER INFORMATION: i
; OTHER INFORMATION: E
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US-08-110-947-10
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                                                  Sequence 10, Application US/08110947 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
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Matches 7; Conserv
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LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/786,648 CURRENT FILING DATE: 2001-03-07 PRIOR APPLICATION NUMBER: PCT/GB99/02970 PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Peptide Fragments TITLE OF INVENTION: Adjuvants FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 45...65
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable OTHER INFORMATION: human variant E. coli
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVPGSQH 7
                                                                                                                                                                                         1 EVPGSQH 7
                                                                                                                                                       EVPGSQH 13
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READ, Randy J
STEIN, Penelope
COCKLE, Stephen
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                              isolated or synthetic {\tt EtxB} beta4-alpha2 loop fragment derivable porcine {\tt E.} coli
                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                             Score 39; DB
Pred. No. 4.4;
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Pred. No.
                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Cholera Toxin B or Enterotoxin B as Vaccine
                                                                                                                                                                                                                                                             DB 21;
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                                                                                                                                                                                                                             0,
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US-08-110-947A-26; Sequence 26, Application US/08110947A; GENERAL INFORMATION:
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TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Compati
                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/110,947A
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                           APPLICANT: COCKLE, Stephen A
APPLICANT: OOMEN, Raymond P
APPLICANT: KLEIN, Michel H
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 1203 Crystal Plaza I, STREET: Davis Hwy.
                                                                                                                                                                                                                      STREET: Suite 1203 Crystal Plaza I, STREET: Davis Highway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038-303 MIS:jb
                                                                                                                                                                 COUNTRY:
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KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                  STEIN, Penelope E
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Shoemaker and Mattare, Ltd.
2001 Jefferson
мынк: US/08/110,947A
24-AUG-1993
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Best Local :
                                                                                   TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
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                                                                                                                                 REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-335
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: DISM PC POOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,121
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
STATE: Ontario
            STRANDEDNESS:
                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/110,947 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                    FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
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nes 7; Conserv
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                      TELEPHONE:
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                                               LENGTH:
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REGISTRATION NUMBER: 2
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M5G 1R7
                             amino acid
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89-9456 LUKPAT
                                              93 amino acids
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Suite 701, 330 Un:
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illarity 100.0%;
Conservative (
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linear
                                                                                                                       (416) 595-1155
            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 University Avenue
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Pred. No. 21;
0; Mismatches
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RESULT 11
US-08-782-832-15
; Sequence 15, Application US/08782832
; GENERAL_IMPORMATION:
Charles J.
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                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                 CORRESPONDENCE ADDRESS
                               TITLE OF INVENTION: PRODUCTION OF AN ORALLY IMMUNOGENIC TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLANUMBER OF SEQUENCES: 17
                                                                          APPLICANT: Arntzen, Charles J. APPLICANT: Mason, Hugh S. APPLICANT: Haq, Tariq A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                    51 EVPGSQH 57
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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ZIP: M5G 1R7
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Zealey, Gavin R.
Klein, Michel H.
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Pravel,
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                                                                                                                                                                                                                                                                                             100.0%;
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Hewitt, Kimball & Krieger
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BER: 1038-417
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Pred. No.
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21;
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Best Local :
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APPLICATION NUMBER: US 08/328,716

FILING DATE: 24-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Denise M.

REGISTRATION NUMBER: 33,924

REFERENCE/DOCKET NUMBER: 36170/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 15:
                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: FOX, David L.
                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/817,906
FILING DATE: 08/04/97
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements, APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NAME: FOX, DAVIG L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          ADDAGE TO STREET: 100 Houston
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 77027-9095
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1301 McKinney, Suite 5100
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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PT; ORGANISM: synthetic construct US-09-836-433-20
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US-09-836-433-14
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
                                                                              Query Match
                                                                                                                                                                                                                                                         Sequence 20, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigego
                                                    Matches
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TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                 TITLE OF INVENTION: HYBREDEPROTEINS FOR AUTOIMMUNE DISEASE FILE REFERENCE: Not Assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
51
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                           1 EVPGSQH 7
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EVPGSQH
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                                                                 Score 39;
Pred. No.
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Pred. No. 23;
0; Mismatches
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Pred. No. 23;
                                                   Mismatches
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RESULT 15 US-09-836-433-22

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Sequence 22, Application US/09836433

GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION UMBER: US/09/836,433
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PRIT
ONG 22
LENGTH: 119
TYPE: PRIT
ORGANISM: Synthetic construct
US-09-836-433-22

Query Match
Dest Local Similarity 100.0%; Score 39; DB 22; Length 119;
Hest Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVPGSQH 7
Db 51 EVPGSQH 57

Search completed: October 24, 2002, 15:30:56
Job time : 49.2787 secs
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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A_Geneseq_032802:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

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11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

25: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

26: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

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71.321 Million cell updates/sec
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41 46	23 26	21	15	15	12	8	7	Length DB
9	16 4	21	16	10	21	21	21	DB
AAP50439 AAP50436	AAR76748 AAP30265	AAY87462 AAY87463	AAR85125	AAP93498	AAY87461	AAY87464	AAY87460	ID
Network polymer wh	Residues 50–64 of Sequence of amino	Cholera toxin B/en E. coli heat labil	Cholera toxin B an	CTP3 epitope of th	Cholera toxin B/en	Cholera toxin B/en	Cholera toxin B/en	Description

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

WPI; 2000-256943/22.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
28	28	28	28	28	28	29	29	29	29	29	29	29	29	29	29	29	29	29	30	30	30	30	30	30	31	33	34	39	39	39	39	39	39
1.	۳	۳,	71.8	۲.	1.	4.	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	٠		76.9		٠								100.0		100.0	100.0
65	58	58	53	39	33	86	86	83	48	29	29	,29	29	29	29	29	29	26	95	93	92	84	79	76	52	15	51	93	93	93	93	93	47
22	21	20	22	22	22	20	20	22	22	22	22	22	22	22	22	22	22	20	22	20	21	22	20	22	22	22	21	22	21	20	20	16	4
AAO10648	AAY70863	AAY05966	AAM83957	AAB31657	AAG76915	AAY07852	AAY07953	AAM89142	AA012358	AAM02658	AAM27359	AAM14930	AAM67068	AAM54665	ABB19338	ABB33898	ABB28719	AAY27825	ABB17963	AAY11752	AAG00632	AAM84660	AAY12891	AA009950	AAU55522	AAB74320	AAG02635	AAB66239	AAY68365	AAW95226	AAY41816	AAR72545	AAP30600
polype	Human tumour antig	Human cancer antig	ĕ	Amino acid sequenc		Human secreted pro	Human secreted pro		Human polypeptide	ide #	#1396	Peptide #1364 enco		Human brain expres	Protein #1337 enco	Peptide #1404 enco	Peptide #1370 enco	Human secreted pro	nervous	Human 5' EST secre	secrete	Human immune/haema	Human 5' EST secre	Human polypeptide	Propionibacterium	Cholera toxin B su	Human secreted pro	-	Heat labile toxin	E. coli heat-labil	Escherichia coli v	osyla	Sequence of amino

ALIGNMENTS

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RESULT 1
AAY87460
ID AAY8
XX AAY8
AC AAY8
XX Chol
XX C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:2
                                                                                                                                                                                                                                                                                    Williams NA, Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200014114-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY87460;
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                                                                                                                                                                                                                                                                                                                                                                                  (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98GB-0019484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB02970
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Claim 1; Page 13;

62pp;

English.

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RESULT 2
AAY87464
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibit of for toxin-induced diarrhoea.
                                             Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind tiglycolipid receptor {\tt GM-1} -
                                                                                                                                                      Williams NA,
                                                                                                                                                                                                                             07-SEP-1998;
                                                                                                                                                                                                                                                               07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin B/enterotoxin B-derived immunomodulatory peptide
                                                                                                                     WPI; 2000-256943/22.
                                                                                                                                                                                                                                                                                                 16-MAR-2000
                                                                                                                                                                                                                                                                                                                                    WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY87464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY87464 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                           (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                        Hirst TR;
                                                                                                                                                                                                                             98GB-0019484
                                                                                                                                                                                                                                                               99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 39; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EtxB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Example

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Page 45; 62pp; English

Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind glycolipid receptor ${\tt GM-1}$ -

Page 15; 62pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY87461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The invention relates to peptide fragments of the Escherichia coli heat CC labile enterotoxin (Etx) and its closely related homologue, cholera CC toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are CC composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention (AXM87461-Y87463) are CC same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may be used as an inhibitor for CC toxin-induced diarrhoea. Therefore, the peptides may be used in the CC production of a composition for treating, preventing and/or modulating a CC diarrhoea. Sequences AXM87464-Y87465 represent peptides used in an CC examplification of the present invention to assess whether a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                  07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention to assess whether a peptide corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB has immunomodulatory effects. Peptide AAV87464 corresponds to residues 51-58 of the EtxB/CtxB beta-4-alpha-2 loop, and peptide AAV87465 is a
                                                                                                      WPI; 2000-256943/22.
                                                                                                                                        Williams NA,
                                                                                                                                                                           (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                07-SEP-1998;
                                                                                                                                                                                                                                                                                     16-MAR-2000
                                                                                                                                                                                                                                                                                                                         WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                               adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY87461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY87461 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 randomly selected control peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                               immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 39; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                          Hirst
                                                                                                                                                                                                                98GB-0019484
                                                                                                                                                                                                                                                    99WO-GB02970
                                                                                                                                           TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No. 6.4e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 4
AAP93498
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                        W08,91.0967A
This sequence corresponds to the CTP3 epitope of the Cholera toxin subunit. The DNA sequence encoding this ligates to othersynthetic oligonuclectides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immunc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                                                  Disclosure;
                                                                                                                                   New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for p
                                                                                                                                                                                                                                      Marjarian WR,
                                                                                                                                                                                                                                                                                       (PRAX-)
                                                                                                                                                                                                                                                                                                                                                      05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP93498 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB)
                                                                                                                                                                                                                                                                      (STRD ) LEYLAND STANDFORD JUNIOR UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope of Cholera toxin B subunit; flagellin fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope of the Cholera toxin B subunit.
                                                                                                                                                                                     1989-356496/48
)B; AAN92414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conser
                                                                                                                                                                                                                                                                                       PRAXIS BIOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                  fig.4B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                      Stocker
                                                                                                                                                                                                                                                                                                                      88US-0190570
                                                                                                                                                                                                                                                                                                                                                        89WO-US01932
                                                                                137pp;
                                                                                                                                                                                                                                    BAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds;
                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                      Newton SMC
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Pred. No. 0.29;
                                                                                                                                 proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                 and for prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 5
AAR85125
ID AAR8
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Best Local Similarity
Matches 7; Conser
                                                      Query Match
Best Local
                                           Matches
                                                                                                                     A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a micropartLoulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                                                 Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                       Sequence
                                                                                                                                                                                                                Claim 7; Page 25; 40pp; English.
                                                                                                                                                                                                                                       aldehyde silica
                                                                                                                                                                                                                                                                                                WPI; 1995-403805/51.
                                                                                                                                                                                                                                                                                                                       Marks
                                                                                                                                                                                                                                                                                                                                                                  03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9529701-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conjugate; cholera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B antigenic peptide fragment CTP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR85125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR85125 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy
                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intestines; antibodies; secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVPGSQH 7
N
                     1 EVPGSQH 7
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                                          Similarity
7; Conserv
                                                                                                             IgA class.
                                                                                                                                                                                                                                                                                                                      Mirelman
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                                                                                         15 AA
                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
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Pred. No. 0.3
); Mismatches
                                                      Score 39;
Pred. No.
                                           Mismatches
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                                                      0.37;
                                                                  DB 16;
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                                                                 Length 15;
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                                           Indels
                                           0;
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                                           Gaps
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RESULT 7
AAY87463
ID AAY8
XX
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                                                                                                                                                                                                                                                     is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-
Cribosyltransferase activity, while the B subunits (EtxB and CtxB)
Cfacilitate the entry of subunit A into the host cell via the binding and
Ccross-linking of GM-1 receptors. Although GM-1 binding is responsible
Cfor some of the effects of Etx and Ctx, it has been found that certain
Cffects of the toxins, such as immunomodulation, are not mediated
Cthrough GM-1 binding. The peptides of the invention are fragments of the
Deta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as
Cnormal EtxB and CtxB subunits, except that they do not bind or cross link
CGM-1. They may be used in medicine as an immunomodulator or adjuvant.
They may also be used as an inhibitor for toxin-induced diarrhoea.
Chert treating, preventing and/or modulating a disease associated with an
Cfor treating preventing and/or modulating a disease associated with an
Cfor treating the peptides of the invention, AAY87460 being
Cparticularly preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                   Matches
AAY87463;
                                AAY87463 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptide fragments of the Escherichia coli he labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-256943/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams NA, Hirst TR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B/enterotoxin B-derived peptide, SEQ
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                                                                                                                                                 1 EVPGSQH 7
                                                                                                                                                                                 Similarity 7; Conserv
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                                                                                                                                                                                   Conservative
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                                                                                                                                                                                               100.0%; Score 39;
100.0%; Pred. No.
                                  21
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                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                 DB 21;
0.52;
                                                                                                                                                                                   0;
                                                                                                                                                                                                                 Length 21;
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                                                                                                                                                                                   Gaps
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RESULT 8
AAR76748
ID AAR7
XX
AC AAR7
XC AAR7
XX
DT 18-M
XX
Resi
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Best Local Similarity
Thes 7; Conserv
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                                                                                                                                                                                                                                                                                                       effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor {\tt GM-1} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain
                                                                AAR76748
                                                                                             AAR76748 standard; Protein;
                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli heat labile enterotoxin B-derived peptide, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000
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                                                                                                                                                                                                          1 EVPGSQH 7
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                23
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                     Score 39;
Pred. No.
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                       DB 2
0.52;
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                                                                                                                                                                                                                                          0,
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                                                                                                                                                                                                                                          0;
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Residues 50-64 of cholera toxin B subunit and FimH 224-226

18-MAR-1996

(first entry)

0

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RESULT 9
AAP30265
ID AAP3
XX
AC AAP3
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                                                                                                                                                                                                       This sequence is encoded by a fragment of the the plasmid pLPA93

C which was used in the production of finh fusion genes comprising

C the cholera toxin B subunit inserted into the finH gene. This insert

C shows the inclusion of the B subunit into the FinH protein at position

C 24-226. The chimeric genes were then opt. further modified by insertion

C of the hepatitis B virus surface antigen pre-S2 region into a different

C position of the FinH adhesin of type I fimbriae. Restiction site handles

C (BgIII-sites) were introduced into the finH gene, and the foreign

C epitopes are then inserted in-frame. In the selected positions the

C insertion of the epitopes did not significantly alter the adhesive

C function of the FinH protein. The expression of the chimeric proteins

C on the surface of fimbriae on bacterial hosts illustrated the possibility

C of using bacterial adhesins as general presenters of foreign antigens and

C pitopes. These chimeric genes may be used in the production of variant

C rimH adhesins which may be useful for targetting active compounds

C and microbial cells to locations comprising selected receptors to which
                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conser
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 AAP30265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor specific bacterial adhesins - useful for targe compounds and microbial cells to locations of receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
Chimeric -
                          AAP30265 standard; Protein; 26 AA
                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hasty DL,
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                                                                                                                                                                                                                               adhesins bind
                                                                                          EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimF; FimG; receptor binding site; PCR; amplify; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae
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                                                                                                                                                 Conservative
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5..19
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20..22
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                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cholera toxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Represents FimH
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                                                                                                                                                 0;
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Pred. No. 0.5
0; Mismatches
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                                                                                                                                                            DB 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit 50-64"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sokurenko
                                                                                                                                                 0
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                                                                                                                                                                        Length
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                                                                                                                                              Gaps
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20-JUN-1985

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RESULT 10
AAP50439
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CNRS )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholera toxin B, medicaments - ef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of amino acids 50-75 of the cholera toxin B1 subunit which carries an Arg at posns. 67 and 73.
                                                                                                                                                                              AAP50439 standard; protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholerae infections, are prepd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera vaccine;
Heat-labile
                                   Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis
                                                                                                  01-JAN-1980
                                                                                                                                          AAP50439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1983-834645/49.
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                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                        1 EVPGSQH 7
                                                                                                                                                                                                                                                                                   EVPGSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNRS
                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-10mg of active cpd
                                                                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raulais D,
A, Delmas
enterotoxin; heat-stable toxin;
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENT NAT RECH
PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B, sub-unit polypeptide(s) as vaccines and
effective against Escherichia coli and Vibrio
ctions, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82FR-0009167
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                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rivaille P,
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                                                                                                                                                                                                                                                                                                                                                              Score 39; DE
Pred. No. 0.6
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
0.65;
vaccine;
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
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RESULT 11
AAP50436
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
             The repeating units are bonded together by intramclecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The
    composite
                                                                                                                                                                                                                                                                                                                            Network polymer labile toxin (L?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New synthetic polypeptide(s) for part of E. useful for vaccination of mammals against t
                                                                       Claim 8;
                                                                                           New synthetic polypeptide(s) for part of E. couseful for vaccination of mammals against the
                                                                                                                             WPI; 1985-159230/26.
                                                                                                                                                Houghten
                                                                                                                                                                                             12-DEC-1983;
                                                                                                                                                                                                                                         20-JUN-1985.
                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                        Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                              01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                   AAP50436;
                                                                                                                                                                                                                                                                                                                                                                                                        AAP50436 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                        (SCRI-)
                                                                                                                                                                                                                   12-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCRI-) SCRIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVPGSQH 7
                                                                                                                                                                       SCRIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
7; Conserv
                                                                                                                                                  RA;
                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                            er which comprises a series (LT)/heat-stable toxin (ST)
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                       100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100; 120pp; English.
                                                                                                                                                                                             83US-0559469
                                                                                                                                                                                                                  84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84WO-US02030
                                                                                                                                                                       CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLINIC RES
                                                                      120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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      made
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DE
Pred. No. 1;
0; Mismatches
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      solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                           of composite E. coli heat-
polypeptide repeating unti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB
                                                                                                      coli enterotoxin(s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
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                                                                                           enterotoxin(s)
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AAP30600
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                                       Query Match
Best Local S
Matches 7
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Best Local S
Matches 7
                                                                                                          The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                  Cholera toxin B, sub-unit polypeptide(s) as vaccines medicaments - effective against Escherichia coli and cholerae infections, are prepd. by solid phase peptic
                                                                                                                                                                                                                                                                           WPI;
                                                                               Sequence
                                                                                                                                                                                                                                                                                              Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of carries an 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant DNA techniques. X9 is Met or X39 is Asn or Tyr and X46 is Tyr or Asn.
                                                                                                                                                                                                                                                                                                       Milhaud G,
                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                          26-MAY-1982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP30600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP30600 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1983;
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                                                                                                    vaccine
23
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                    <del>ب</del>
EVPGSQH
                   EVPGSQH
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                                       Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                              Page 11; 13pp; French.
                                                                                                   1-10mg
                                                                                47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg
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Arg at
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A, Delmas A;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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 29
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                                                                                                    of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; E.coli infection;
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                                                                                                    active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                Score 39;
Pred. No.
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Pred. No.
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                                         Mismatches
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See also AAP50439-57.
                                                           4.
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                                                                                                                                                                                                                                   peptide synthesis
                                                          Length 47;
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                                         Indels
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Vibrio
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                                        Gaps
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RESULT 14
AAY41816
ID AAY41
XX
AAY41
XX
AC AAY41
XX
DT 08-DE
DX 08-DE
CXX
DE Esche
XX
ADP-1
KW ADP-1
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AAR72545
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Best Local :
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                                                                                                                                                                                                                                                                                                             New modified forms of pertussis holotoxin - crystalline forms of pertussis holotoxin and
 Escherichia coli
                 three-dimensional
                        ADP-ribosylating
                                        Escherichia
                                                         08-DEC-1999
                                                                                       AAY41816 standard; peptide; 93
                                                                                                                                                                                                                                                                                                                                      WPI; 1995-132623/18.
                                                                                                                                                                                                                                                                                                                                                     Armstrong GD,
Oomen R, Read
                                                                        AAY41816;
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                     Disclosure; F1g 5; 54pp;
                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP646599-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR72545 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR72545;
                                                                                                                                                                                                                pertussis
                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB (UYAL-) UNIV ALBERTA.
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                                                                                                                                                               Local Similarity res 7; Conserv
                                                                                                                               41 EVPGSQH 47
                                                                                                                                               1 EVPGSQH 7
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                                                                                                                                                                                                               infection.
                                                                                                                                                                                                93
                                        coli verotoxin-1
                                                                                                                                                                Conservative
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                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                    Cockle SA,
RJ, Stein
                                                                                                                                                                                                                                                                                                                                                                                                     93US-0110947
94US-0251121
                                                                                                                                                                                                                                                                                                                                                                                                                              94EP-0306219
               toxin; PT; crystalline pertussis holotoxin; l structure; LT; immunoprotective; infection
                                                                                                                                                                                                                       in the development of vaccines against Bordetella
                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     LTD
                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                             Hazes B,
                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                        B-subunit.
                                                                                                                                                              Score 39; DE
Pred. No. 2.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                     developed using
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AAW95226
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Matches
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Hazes B,
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US5856122-A
                                                                                                       AAW95226;
                                                                                                                      AAW95226
                                                                                                                                                                                                                               Sequence
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holotoxin, functional (au) .....holotoxin, functional (au) holotoxin, functional (au) holotoxin, functional to pertussis holotoxin can be identified. This can be pertussed by the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating holotoxin. The present sequence represents an ADP-ribosylating the present besubunit peptide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:
(1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the
                                                                    Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                structural analysis;
heat-labile; LT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystalline holotoxin, in relation to known information of the
Escherichia coli
                                                                                                                                                                      E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                      16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 5; 41pp;
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05-JAN-1999.

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Search completed: October 24, 2002, 15:35:01 Job time: 12.9016 secs
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                                                                                                                                                                                                             The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying CC at least 1 site in a PT that interacts with a molecule that is capable of CC forming a complex with the holotoxin and which molecule is an effector CC molecule which is an adenine nucleotide and which site contributes to CC toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional CC structure of crystalline PT, determined by X-ray crystallogaphy. The CC identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a CC biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure CC of PT have functional and/or structural resemblance to other bacterial CC toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the CC heat-labile toxin of E. coli (LT) and verotoxin-1. (VT). The present CC sequence represents the beta-subunit of LT toxin.
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Matches 7
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24-AUG-1993;
31-MAY-1994;
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ld RJ, Stein
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Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/1/
3: /cgn2_6/ptoda+a/1/
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-467-974-26
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US-09-080-023-15
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US-08-258-851-7
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US-09-033-212-6
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US-09-139-802-19
US-08-47-410-12
US-08-481-19-56
US-08-481-813-58
US-08-481-196-8
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(without alignments)
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Patent No.
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Sequence 80		Sequence 62	Sequence 11	Sequence 33	Sequence 33	Sequence 33	Sequence 33	Sequence 12	Sequence 3,	Sequence 59	Sequence 59	Sequence 23	Sequence 23	Sequence 23	Sequence 23	Sequence 16	Sequence 16
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ALIGNMENTS

APPLICATION NUMBER: US/08/292,968
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION NUMBER: US 08/251,121
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTONNEY/AGENT INFORMATION:
NAME: STEWART, Michael I:
REGISTRATION NUMBER: 1038-388
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-115 COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 93 amino acids TYPE: amino acid STRANDEDNESS: single TITLE OF INVENTION: MO NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: INFORMATION: CANT: READ, Randy J. Application US/08292968 Suite 701, 330 University Avenue STEIN, Penelope E COCKLE, Stephen A OOMEN, Raymond P. (416) 595-1163 HAZES, Bart LOOSMORE, Sheena KLEIN, Michel H. ARMSTRONG, Glen D. linear Sim & McBurney MODIFICATION OF Release #1.0, Version PERTUSSIS #1.25

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US-08-467-974-26
                                                                                                                                 INFORMATION FOR SEQ ID NO: 26.
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino
                                                           Query Match
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Best Local :
                                   Matches
                                                   Best
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC-DOS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
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Patent No. 5
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APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
APPLICATION DATA: US 08/251,121
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                            FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                Local Similarity
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/467,974 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
les 7; Conservative
                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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    EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08467974
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Suite 701, 330 University Avenue
                                   Conservative
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                                                                                                         SS: single
linear
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ARMSTRONG, Glen D.
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                            100.0%; Sc
100.0%; P:
ative 0;
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                            US 08/110,947
                                                                                                                                                                                                                                                                24,973
                                                                                                                                                                                                                                                 1038-454 MIS:vg
                                                Score 39; DB 2; Pred. No. 0.67;
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Pred. No. 0.67;
                                 Mismatches
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                                                           Length 93;
                                 Indels
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                                 Gaps
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                                0;
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                                            RESULT 4
US-08-467-976-26
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Sequence 26, Application US/08467976 Patent No. 6018022 GENERAL INFORMATION:
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US-08-467-536-26
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US-08-467-536-26
                                                                Matches
                                                                                            Query Match
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COUNTRY: Canada
2IP: M5G 1R7
COMPUTER READABLE FORM:
COMPUTER FLOPPY disk
                                                                                                                                                                                                                         TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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APPLICANT:
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CITY: Toronto
STATE: Ontario
11|||||
41 EVPGSQH 47
                                                                                                                                                           LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                             Local Similarity nes 7; Conserv
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                  NAME: STEWART, Michael I. REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0: FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPUID: TYPE: Floppy ----
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
CVCTEM: PC-DOS/MS-DOS
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                               1 EVPGSQH 7
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5977304
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                                                              100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                             linear
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ite 701, 330 University Avenue
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06-JUN-1995
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                                                                0;
                                                              Score 39; DB Pred. No. 0.6
                                                                             DB 2; Length 93; 0.67;
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                                                                Indels
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Best Local Similarity
7; Conserve
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                                                                                                                                     Sequence 26, Application US/09082514
Patent No. 6168928
GENERAL INFORMATION:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
APPLICATION NUMBER: US 08/251,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
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MEDIUM TYPE: Floppy disk
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TITLE OF IN
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APPLICANT:
                APPLICANT:
TITLE OF I
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REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Sim & McB
                                               APPLICANT:
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                                                                                                                                                                                                                                                   41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
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M5G 1R7
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                INVENTION:
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SEQUENCES:
                                        STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P. KLEIN, Michel H. ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 701, 330 University Avenue
                                                                                                                         READ, Randy J.
                                                                                                                                                                                                                                                                                                               Conservative
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                             HAZES, Bart
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PC-DOS/MS-DOS
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MODIFICATION OF PERTUSSIS TOXIN 46
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                                                                                                                                                                                                                                                                                                                                         Length 93;
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CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 93
TYPE: PRT
RCANISM: Homo saplens
US-09-069-023-15
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US-09-069-023-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09069023A Patent No. 6348573
                                                           Matches
                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                            APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
Sim & McBurney
Thor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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41 EVPGSQH
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2 MPGSQH
                           2 VPGSQH 7
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                                                                          Similarity
                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                          79.5%;
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                                                                        Score 31;
Pred. No.
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Pred. No. 0.67;
                                                           Mismatches
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                                                                                        DB
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                                                                                        Length 93;
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US-08-258-851-7
; Sequence 7, Application US/08258851
; Patent No. 5585244
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                                                                                                                                                                                                       RESULT 9
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US-09-031-962D-20
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US-09-450-072-78
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SEQ ID NO 20
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Delcayre, Alain
APPLICANT: Delcayre, Alain
TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune:
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000,1042c1
CURRENT APPLICATION NUMBER: US/09/450,072
CURRENT APPLICATION NUMBER: 09/351,348
EARLIER APPLICATION NUMBER: 09/351,348
EARLIER FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 81
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09031962D Patent No. 6350867
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                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/031,962D CURRENT FILING DATE: 1998-02-27 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Osseous Growth, Repair, and R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas C. Hart APPLICANT: Jennifer A. Price
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                             APPLICANT: Elizabeth A. Allegretto
APPLICANT: J. Wesley Pike
TITLE OF INVENTION: DETECTION OF RET.
TITLE OF INVENTION: RECEPTOR SUBTYPE
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 39
CORRESPONDENCE
                 NUMBER OF SEQUENCES:
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Local Similarity 66.7%;
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                                                                       DETECTION OF RETINOID
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1; Mismatches
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Pred. No.
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RESULT 10
US-07-789-912-5
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GENERAL INFORMATION:
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 14 AMINO ACIDS
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,912
FILING DATE: 19911104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
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CITY: LOS Angeles

STATE: California
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHAMBON, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/258,851 FILING DATE: 10 June 1994 CLASSIFICATION: 435
                                                                                                                                                                           ZIP: 20036
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TELEFAX: (213) 955-0440
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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STREET: 611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                              Application US/07789912
                                                                                                                                                                                                                                                  E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Ave. NW Suite 300
                                                                                                                                                                                                USA
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83.3%;
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Pred. No.
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ATTORNEY/AGENT INFORMATION:

FILING DATE:

APPLICATION NUMBER:

US 07/581,694

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Sequence 6, Application US/09003708A
Patent NO. 6010882
GENERAL INFORMATION:
APPLICANY: WU, Jen-Leih
APPLICANY: CHEN, Jyh-Yih
APPLICANY: CHEN, Jyh-Yih
APPLICANY: CHANG, Chi-Yaco
TITLE OF INVENTION: Production of I
TITLE OF INVENTION: Polypeptides
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US-09-003-708A-6
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Best Local S
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TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 5:
             TELEFAX: (202)-347-787:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003
FILING DATE: 01/07/98
                                                              REGISTRATION NUMBER: 24,962
REFERENCE/DOCKET NUMBER: ACJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-347-2600
TELEPAX: (202)-347-7870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
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FILING DATE: January 10, 1997
ATTORNEY/AGENT IMFORMATION:
NAME: Ronald R. Snider
                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette MEDIUM TYPE: storage
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les 5; Conserv
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amino acid
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P.O. Box 27613
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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83.3%;
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                                                                                                                   ACA-001
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Pred. No. 23;
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-09-003-708A-6
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; HYPOTHETICAL:
US-09-383-212-6
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Best Local :
                                                                        Query Match
Best Local Similarity
                                                          Matches
                                                                                                                                                                                                                       TELEFAX: (202)-347-78
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 43,538
REFERENCE/DOCKET NUMBER: ACA-001-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)-347-2600
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/003,708
FILING DATE: 01/07/98
APPLICATION NUMBER: 60/034/736
FILING DATE: January 10, 1997
APPLICATION NUMBER: 09/03/708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                FILING DATE: January 7, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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APPLICANT: CHEN, Jyh-Yih
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 71.4 hes 5; Conservative
                                                                                                                                                             LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 20038
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20 EVPKKQH 26
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                             EVPGSQH 7
                                                                                                                                                                                                                                                                                                                  Fei-Fei Chao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Snider & Chao, L.L.P. P.O. Box 27613
                                                                                                                                                                                                                                       (202)-347-7870
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71.4%;
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71.48;
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Pred. No. 1.
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US-08-747-410-12
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US-09-139-802-193
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                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,4:
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
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APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: MGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
FILLE OF INVENTION UNMEER: US/09/139,802
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER APPLICATION NUMBER: 08/910
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1996-09-10
EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
COUNTAINER: DESCRITA US: 23
COUNTAINER: DESCRITA 
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                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
TELECOMMUNICATION INFORMATION: TELEPHONE: 612/371-5268
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
                                                                        REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3100 No. : CITY: Minneapolis
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Pred. No. 1.7e+05;
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US-08-260-582-56
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: G1 5236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
                              Matches
                                                         Query Match
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                             Best Local Similarity Matches 5; Conserv
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Matches 5; Conserv
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MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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STATE: Massachus
COUNTRY: U.S.
                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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 2 VPGSQ 6
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Pred. No.
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27;
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24;
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Search completed: October 24, 2002, 15:38:21 Job time : 5.01639 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length:
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1: /cgn2_6/ptodata/1/paa/Pc

2: /cgn2_6/ptodata/1/paa/Us

3: /cgn2_6/ptodata/1/paa/Us

4: /cgn2_6/ptodata/1/paa/Us

5: /cgn2_6/ptodata/1/paa/Us

6: /cgn2_6/ptodata/1/paa/Us

6: /cgn2_6/ptodata/1/paa/Us

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10: /cgn2_6/ptodata/1/paa/Us

11: /cgn2_6/ptodata/1/paa/Us

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39
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Match Length
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Gapop 10.0 ,
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US-08-110-947-10
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52.884 Million cell updates/s
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Sequence
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Sequence 3
Sequence 1
Sequence 1
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	21 US-09-760-495-	96	76.9	30	41
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	13 US-08-905-144-35	9:	76.9	30	38
	26 US-60-194-243-2	90	5	30	7
	26 US-60-192-73	9(76.9	30	36
	26 US-60-173-465-5	9	6	30	ű
Sequence 4087,	26 US-60-188-162-4	8	9	30	4
	24 US-10-092-399-1	8,	76.9	30	33
Sequence 1225	21 US-09-764-905-1	8,		30	32
_	1 PCT-US01-01354-1225	8	76.9	30	31
	26 US-60-194-243-	8	6	30	30
	26 US-60-192-739-2	8	76.9	30	29
	26 US-60-186-656-100	00	5	30	8
48	13 US-08-905-279-	79	76.9	30	27
Sequence 1575	20 US-09-688-051-15	7	76.9	30	6
	26 US-60-173-465-44	7:	٥,	30	25
Sequence 752,	21 US-09-757-034-75	6	6	30	24
Sequence 2956,	26 US-60-178-308-29	5	6	30	ũ
470	19 US-09-595-298A-47	. و	9	31	Ñ
Sequence 8, Appl	26 US-60-112-736-	7.	9	31	21
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e 296	20 US-09-688-051-29	4.	7.	34	0
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ALIGNMENTS

US-09-786-648-2

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PERMITH: 7
PRE: PRT
ORGANISM: E. CO11
FEATURE:
LOCATION: 51...57
OTHER INFORMATION: 1
OTHER INFORMATION: 1
US-09-786-648-2
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                                 Query Match
Best Local S
Matches 7
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SOFTWARE: MS DOS
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09786648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                 Local Similarity 100 nes 7; Conservative
 1 EVPGSQH 7
                                                                                                                   isolated or synthetic human variant E. coli
                                               100.0%;
                                   0;
                                 Score 39; DB Pred. No. 3.2 0; Mismatches
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RESULT 3
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GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
APPLICATION NUMBER: IL 109519
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MIRELM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PC7/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond
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OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                      APPLICATION NUMBER: US/08/732,371
FILING DATE: 09-JAN-11997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST TITLE OF INVENTION: INFECTING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARKS, Robert
SELA, Michael
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                                                                       Query Match
Best Local
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                                                           Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,371A
FILING DATE: 09-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109519
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: MIRELM
                                                                                                                                                                                                      TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                  TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES F
TITLE OF INVENTION: INFECTING
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                 MOLECULE TYPE:
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                                                      Local Similarity tes 7; Conserv
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2 EVPGSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                            1 EVPGSQH 7
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                          15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIRELMAN, David
                                                           Conservative
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                                                                                                                                 protein
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                                                                    100.0%;
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Pred. No.
                                                                        Score 39;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENTS
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                                                           Mismatches
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RESULT 5 US-09-786-648-4

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APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Chc
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 74.8
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 199-09-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEG ID NO 4
LENGTH: 21
                                                                                 RESULT 7
US-08-110-947-10
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GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                   Sequence 10, Applicat GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: E. FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 21
TYPE: PRT
ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 45...65
OTHER INFORMATION:
OTHER INFORMATION:
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                   APPLICANT:
                                     APPLICANT:
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nes 7; Conserv
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nes 7; Conser
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                                                                    Application US/08110947
READ, Randy J
STEIN, Penelope
COCKLE, Stephen
                                                                                                                                                                                                                                                                                                                                                                                 coli
                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                            isolated or synthetic EtxB beta4-alpha2 loop fragment derivable porcine E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated or synthetic EtxB beta4-alpha2 loop fragment derivable human variant E. coli
                                                                                                                                                                                                                         100.0%; S
100.0%; F
tive 0;
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                                                                                                                                                                                                                         Score 39; DB 2
Pred. No. 4.4;
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                         DB 21;
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TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,947A
APPLICATION NUMBER: US/08/110,947A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSEE: Shoemaker
                                                                                                                                                                                                                                                                                                                   APPLICANT: READ, Randy J
APPLICANT: STEIN, Penelope
APPLICANT: COCKLE, Stephen
APPLICANT: COMEN, Raymond P
APPLICANT: KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1038-303 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                          ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203 Crystal Plaza I, 20
STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Shoemaker and Mattare, InstreET: Suite 1203 Crystal Plaza I, STREET: Davis Hwy.
                                                                                                                                                                     CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVPGSQH 7
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                                                                                                                                        22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 amino acids
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KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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Pred. No.
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Mismatches
                                          Version
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CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:

FALLOW,

Charles W

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US-08-251-121-26
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                                                                                                                                                                                                                                                                                                                                                      STATE: Ontal
COUNTRY: Canada
2IP: M5G 1R7
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
MEDDIUM TYPE: IBM PC compatible
TWENTEM: PC-DOS/MS-DOS
T-lease #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08251121 GENERAL INFORMATION:
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                                                                                                     INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038-303 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
TELEPAX: 89-9456 LUKPAT
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/110,947 FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                             LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1994
                                                                                                                                                                     REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-335
                                                                                                                                                                                       NAME: STEWART, Michael REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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Local Similarity 100.0%;
les 7; Conservative (
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P.
                                                                                                                    (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
              linear
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                                                                                                                                    (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Randy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                               US/08/251,121
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Pred. No.
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Mismatches
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Query Match
Best Local Similarity
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Sequence 5651, Application US/096; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
                                                                               ; OTHER INFORMATION: Ceres Seq. US-09-617-682A-5651
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Best Local Similarity
7; Conserv
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                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/617,682A
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 16871
SEQ ID NO 5551
LENGTH: 84
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/688,051
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 4193
SEQ ID NO 2967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2967, Application US/09688051 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                          APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2750-1242P
                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..84
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..41
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..41
LOCATION: 1..41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 41
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                              NAME/KEY: misc_feature LOCATION: 1..84
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Ceres Seq. ID 1714257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                Conservative
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                              87.2%;
71.4%;
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71.4%;
               Score 34; DB 20;
Pred. No. 1.7e+02;
2; Mismatches 0
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                                                                                               ID 1355962
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Pred. No.
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Pred. No.
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                                            Length 84;
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                Indels
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                0;
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                Gaps
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                0;
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KIPGSQH 58

us-09-866-066-35

Sequence 35, Application US/09866066 GENERAL INFORMATION:

APPLICANT: Benjamin, Christopher APPLICANT: Roberds, Steve

APPLICANT:
APPLICANT:
APPLICANT:

CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/207,152
PRIOR FILING DATE: 2000-05-26

APPLICANT: Ruble, Cara
APPLICANT: Gottow, Lisa
APPLICANT: Karnovsky, Alla
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00229 US1
CURRENT APPLICATION UMMBER: US/09/866,066
CURRENT FILING DATE: 2001-05-23

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RESULT 13
US-60-192-587-1036
US-60-192-587-1036
; Sequence 1036, Application US/60192587
; GENERAL INFORMATION:
; GENERAL SECTION OF THE SECT
RESULT 14
US-60-194-091-1018
; Sequence 1018, Application US/60194091
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
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Best Local Similarity
5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/192,587
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 1666
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1036
LENGTH: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: CL000405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/207,257
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,119
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 42
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42 EIPGFQH 48
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Pred. No. 3e+02;
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Pred. No. 1.5e+02;
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US-08-888-755-16
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Best Local Similarity
"" hes 5; Conserv?
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CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 1598
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08888755 GENERAL INFORMATION:
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: CL000416
                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RUSSELL, JC
APPLICANT: Colpitts, T
TITLE OF INVENTION: RE
TITLE OF INVENTION: FC
                                                                                            TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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|:|| ||
42 EIPGFQH 48
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                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                           TELEFAX: 847/938-2623
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                Conservative
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                            79.5%;
83.3%;
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71.48;
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             Score 31; DB 12;
Pred. No. 2.9e+02;
1; Mismatches 0
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Pred. No. 3e+0
1; Mismatches
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                                             Length 41;
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                Indels
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Search completed: October 24, 2002, 15:45:14 Job time : 48.5902 secs

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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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   length:
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
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Gapop 10.0 ,
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Maximum Match 100%
Listing first 45 summaries
 EVPGSQH 7
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   2002, 15:35:39 ;
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               US-10-212-759-1554
PCT-US02-09921-833
US-10-235-954-759
US-09-547-599C-2880
US-09-547-799C-248
US-10-182-995-21108
US-10-182-995-2170
US-10-182-997-1975
US-10-182-997-1975
US-10-182-997-1975
US-10-182-997-1975
US-10-182-998-11398
US-10-203-135-26391
US-10-203-135-26391
US-10-203-137-27628
US-10-203-139-26533
US-10-105-730-115
US-10-106-698-7689
US-10-106-698-7689
US-10-106-698-797
US-10-107-79-78
US-09-807-512-10
US-10-235-941-2637
US-10-235-951-2633
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(without alignments)
137.008 Million cell updates/sec
sequence
2480, Ap

583, App

21108, A

2737, A

26770, A

11398, A

11398, A

11398, A

11398, A

115, App

2653, App

2169, App

210, App

10, App
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Matches 5
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US-10-106-698-6636	us-10-106-698-6626	US-10-106-698-8340	US-10-106-698-6634	US-10-106-698-8458	US-10-106-698-8196	US-10-106-698-6618	US-10-106-698-5746	US-10-040-394-15	us-10-106-698-7879	US-10-106-698-6637	US-10-106-698-6612	US-10-106-698-6607	US-10-106-698-6625	US-10-106-698-6604	US-10-106-698-8197	us-10-062-831-123	US-10-235-953-3641	US-10-155-881-12211
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence							
6636,	6626,	8340,	6634,	8458,	8196,	6618,	5746,	15, Ap	7879,	6637,	6612,	6607,	6625,	6604,	8197,	123, A	3641,	12211,
Āρ	Αp	App1	Αp	App	Αp	A												

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/212,759
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: 09/758,446
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1734
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1554
LENGTH: 64
RESULT 2
PCT-US02-09921-833
; Sequence 833, Application PC/TUS0209921
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                              US-10-212-759-1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us-10-212-759-1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1554, Application US/10212759
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM019C1N
                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature LOCATION: (2)
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (16)
                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals
                                                                                                                                                                                               Local Similarity
                                                                                                                 54 VPGSEH
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                                                                                                                 59
                                                                                                                                                                                 Conservative
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83.3%;
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Anissa L.

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APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PM002CIN

CURRENT APPLICATION NUMBER: US/10/235,954

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: 09/757,034

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR APPLICATION NUMBER: 2001-02-04
                                                                                                                                                                                                         US-10-235-954-752; Sequence 752, Applic: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LI:036747.17.orf2:2001MAY17
PCT-US02-09921-833
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
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CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;

60/291,829; 60/299,428; 60/300,001; 60/299,776

PRIOR FILING DATE: 2001-03-29; 2001-05-16; 2001-05-17;

PRIOR FILING DATE: 2001-03-29; 2001-05-16; 2001-05-17;

PRIOR FILING DATE: 2001-06-19; 2001-06-20; 2001-05-16; 2001-05-17;

NUMBER OF SEQ ID NOS: 1146

SOFTWARE: PERL Program

SEQ ID NO 833

LENGTH: 82
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TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT-1232 PCT
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24 VPGTQH'29
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HARRIS, Bernard
FLORES, Vincent
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DAHL, Christopher R.
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SON, Olivia
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R, Scott R.
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TY, Sean C.
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83.3%;
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Pred. No.
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 752
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-235-954-752
RESULT 5
US-09-547-599C-2428
; Sequence 2428, Application US/09547599C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Ba
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent.pm
SEQ ID NO 2880
LENGTH: 79
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PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR APPLICATION NUMBER: US 08/905,79
PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR APPLICATION NUMBER: US 08/904,468
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
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Best Local Similarity
Matches 5; Conserv
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Best Local :
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APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: Expressed Sequence Tags and
FILE REFERENCE: GEN-T119C1
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ORGANISM: Homo Sapiens
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OTHER INFORMATION: score 4.60
OTHER INFORMATION: seq CALSLPDAPGASG/GR
                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: -55..-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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nes 5; Conserv
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Pred. No. 1.5e+02;
0; Mismatches 1
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. 1.3e+02;
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Milne Edwards, Jean Baptiste

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RESULT 6
US-10-143-775-583
Query Match
Best Local Similarity
""+ Ches 5; Conserv?
                                                                      ; ORGANISM: Homo sapiens US-10-143-775-583
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                                                                                                                                                                                                                                                                 Sequence 583, Applic GENERAL INFORMATION:
                                                                                                                               Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 1064
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 583
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 5; Conserv
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
FILE REFERENCE: GEN-T119C1
CURRENT APPLICATION NUMBER: US/09/547,599C
CURRENT FILING DATE: 2000-04-11
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/143,775
CURRENT FILING DATE: 2002-05-14
                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC021C1N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SIGNAL LOCATION: -60..-1 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                     LENGTH: 96
TYPE: PRT
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OTHER INFORMATION:
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OTHER INFORMATION: Normal
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ENGTH: 93
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FILING DATE: 1997-08-01
APPLICATION NUMBER: US 08/905,051
FILING DATE: 1997-08-01
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            76.9%; Solilarity 100.0%; I Conservative 0;
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100.0%; Pr
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                           Score 30;
Pred. No.
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Pred. No.
               Mismatches
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       DB 6; Lc. 1.8e+02; 0;
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                                                                                                                                                                           or Palm
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                                       Length 96;
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US-10-203-134-27374
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Sequence 27374, Application US/10203134 GENERAL INFORMATION: APPLICANT: Molecular Dynamics, Inc.
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LENGTH: 29
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GENERAL INFORMATION:
APPLICANT: Molecular Dynamics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                            APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
FILE REFERENCE: PB 0004 WO 6
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
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PRIOR FILING DATE: 27 September 2000 (2)
PRIOR APPLICATION NUMBER: US 60/234,687
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207.456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2002-08-02
CURRENT APPLICATION NUMBER: US/10/203,134
CURRENT FILING DATE: 2002-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: EST_HUMAN HIT: BF063046.1, EVALUE 1.00e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO AC009948.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21108, Application US/10182995
                                                                                                                                                                         Penn, Sharron G. Rank, David R.
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Chen, Wensheng
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Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISSPROT HIT:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - 2000 (27.09.00)
1/234,687
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79;
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                                                          SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 27380\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 27374
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN ADD
FILE REFERENCE: PB 0004 WO 3
                                                                                                    PRILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38578
                                                                                                                                                                        PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
                                                                                                                                                                                                                                           PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 30 June 2000 (30.06.)
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ORGANISM:
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OTHER INFORMATION:
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Local Similarity 66.78;
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 27 September 2000 (27.09.00)
APPLICATION NUMBER: US 60/234,687
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Homo
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Rank, David R.
Hanzel, David K.
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sapiens
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2000 (26.05.00)
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ry 2000 (04.02.00)
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Pred. No.
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ULT LIVER
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PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 03 August 2000 (03.08.00)

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 30 June 2000 (30.06.00)
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                                                                                 Matches
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
FILE REFERENCE: PB 0004 WO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 30 June NUMBER OF SEQ ID NOS: 37811
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                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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OTHER INFORMATION: MAP TO AC009948.2
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  4 IPGEQH
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                                        2 VPGSQH 7
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                                                                                                      Similarity
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    9
                                                                                   Conservative
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l, David K.
                                                                                                                                                                                                                          EST_HUMAN HIT: BF063046.1, EVALUE 1.00e-09
                                                                                                                                                                                        SWISSPROT HIT: P16258, EVALUE 1.60e+00
                                                                                                                                                                                                                                                                     EXPRESSED
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                                                                                                    74.48;
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; Pred. No. 79;
1; Mismatches
                                                                                 Score 29; DB Pred. No. 79; 1; Mismatches
                                                                                                                                                                                                                                                                     IN BRAIN, SIGNAL
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                                                                                                                       Length 29;
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CURRENT APPLICATION NUMBER: US/10/182,998
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HBL 100
FILE REFERENCE: PB 0004 WO 9
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NUMBER OF SEQ ID NOS: 26941

SOFTWARE: Molecular Dynamics Sequence Listing Engine
1EQ ID NO 19756
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Molecular Dynamics, Inc.
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CURRENT FILING DATE: 2002-08-02
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OTHER INFORMATION: MAP TO AC009948.2
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OTHER INFORMATION:
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Hanzel, David K.
Chen, Wensheng
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66.78;
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Pred. No.
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PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207.456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632.366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
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Best Local Similarity
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PRIOR FILING DATE: 27 September ?^^^
PRIOR APPLICATION NUMBER: US 60/236,359
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                        LENGTH: 2'
TYPE: PRT
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
OTHER INFORMATION: EST_HUMAN HIT: BF063046.1, EVALUE 1.00e-09
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Chen, Wensheng
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                                       EXPRESSED IN LUNG, SIGNAL = 1.4
                                                                               MAP
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66.78;
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No.
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US-10-203-138-11687; Sequence 11687, Application US/10203138; GENERAL INFORMATION:
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LENGTH: 29
TYPE: PRT
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Best Local
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                    APPLICANT:
                                                     APPLICANT: Molecular Dynamics,
    APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.0
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2002-08-02
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OTHER INFORMATION:
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OTHER INFORMATION: MAP TO AC009948.2
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Hanzel, David K.
Chen, Wensheng
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Rank, David R.
Penn, Sharron G.
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Hanzel, David K.
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66.78;
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                                                                                                                                                                                                                                                                                               Score 29;
Pred. No.
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Qy
Search completed: October 24, 2002, 15:47:33 Job time: 16.2623 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 15438

SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 11687
                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                              Matches
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2002-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 WO 8
                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: EST_HUMAN HIT: BF063046.1, EVALUE 1.00e-09
                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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A; Experimental source:
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A; Residues: 1-97 < KUR>
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                      5; Conserv
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ALIGNMENTS

C; Accession: S25719
R; Shen, P.; Howlett, G.J.
Arch. Biochem. Biophys. 297, 345-353, 1992
A; Title: Two coding regions closely linked
A; Reference number: S25719; MUID:92359549
A; Accession: S25719 hypothetical protein BMEII0058 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3516
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Iva; RMEZUR, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella me A; Reference number: AD3252; PMID:11756688
A;Accession: AH3516
A;Accession: AH3516
A;Accession: AH3517
A;Status: preliminary A:Status: preliminary A;Molecule type: mRNA A;Residues: 1-75 CSHES-A;Cross-references: EMBL:X56190; protein ECL - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 05-Nov-1999 Conservative Conservative GB:AE008918; PIDN:AAL53299.1; PID:g17984183; GSPDB:GN00191 ce: strain 16M 69.2%; 83.3%; 71.8%; 66.7%; NID:g56075; Score 27; DB Pred. No. 1.1e 0; Mismatches 0; Score 28; DB Pred. No. 85; 2; Mismatches facultative intracellular pathogen Brucella melit ő DB 2; лв ∠, ⊥.1e+02; 1; PIDN:CAA39653.1; the 2 rat apolipoprotein E gene: nucleoti ; Length 97; Length 75; Indels Indels PID:g56076 0; 0; Gaps Gaps 0; 0 Ivanov D.; Let

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hypothetical protein C54G10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20227
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A;Molecule type: DNA
A;Residues: 1-87 <ROG>
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                                  A; Molecule type: DNA
A; Residues: 1-93 <WIL>
                                                                                  A; Reference number: A; Accession: T20227
                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tat protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
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A; Reference number: Z15586
A; Accession: T06281
A; Experimental
                                                                A; Status: preliminary; translated
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A; Residues: 1-87 <ALI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Alizon, M.; Wain-Hobson, S.;
Cell 46, 63-74, 1986
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A;Experimental source: cultivar H722; tissue-type leaf
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              Cross-references: EMBL: Z75532;
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66.7%;
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                PIDN:CAA99809.1; GSPDB:GN00023; CESP:C54G10.1
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A;Title: Nucleotide seguence and expression of Escherichia coli trpR, the structural A;Reference number: A93867; MUID:81175101
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warre adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Gene: CESP:C54G10.1
A;Map position: 5
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                  A; Map position: 100 min
A; Start codon: GTG
                                                                                                                                                                                              A;Cross-references:
C;Comment: This is 1
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A; Residues: 1-66 <STO>
A; Cross-references: GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Complete genome sequence of Pseudomonas A; Reference number: A82950; MUID: 20437337 A; Accession: D83599
                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-33 <GUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-73 <SIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A93698; MUID:81053831
A;Accession: C93698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: DNA sequence of the Escherichia coli trpR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Singleton, C.K.; Roeder, W.D.; Bogosian, Nucleic Acids Res. 8, 1551-1560, 1980
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C; Species: Pseudomonas aeruginosa
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                                                             Query Match
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     4; Conserv
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                                                                                                                                                                                              es: GB:J01715; GB:V00369; NID:g148059 is the hypothetical translation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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           Conservative
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ce: strain PAO1
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57.1%;
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        Score 26; DB
Pred. No. 1.76
1; Mismatches
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No.
DB 2;
1.5e+02;
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1.3e+02;
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hypothetical protein BH2324 [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_chan C;Accession: D83940 R;Takani, Y.; Maeno, G.; Sasaki, R. R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R. Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacteri A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                 RESULT 10
D83940
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Nature 406, 959-964, 2000
A;Title: Complete ...
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A; Residues: 1-84 <GR
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17876
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A; Residues: 1-74 <STO>
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e: specific h
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317-4331, 2000
sequence of the alkaliphilic bacterium
50; MUID:20512582; PMID:11058132
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host Chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB Pred. No. 1.7e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
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1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:AAC96744.1
strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 84;
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                                                                                                                           R.;
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                                                                                                                                                                                                                                                                              (strain C-125)
                                                                                                                       Masui, N.; Fuji,
                                                   Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Larbig,
                                                   halodurans
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K.; L
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                                                   and
                                                                                                                               Hira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Rv2561 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: E70728 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; HG; Connor, R.; Davies, R.; Devlin, R.; Gentles, R.; Gentles, R.; Devlin, R.; Gentles, R.; Devlin, R.; Gentles, R.; 
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E70728
                                               A; Experimental source: C; Genetics: A; Gene: Rv2561
                                                                                                                                                                                                                                                                                                                                                                                                                         Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whit
                                                                                                                                                                                                                                      A;Status: preliminary;
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                         A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987 A;Accession: E70728
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                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-97 <COL>
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GB:Z77250; ce: strain H

; GB:AL123456; H37Rv

NID: g3261617;

PIDN:CAB01043.1; PID:e25531

nucleic acid

sequence

not

shown;

translation

not

Whitehead, S. tuberculosis

from the c

complete B.G s

geno

Skelton, S.;

Squares,

Holroyd,

Gordon

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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wooderage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; I ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AF3175
                                                                                                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; PMID:11743193
A;Accession: AF3175
                                                                                                                                                                                                                                                                                                                                                           attachment protein [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-C;Accession: AF3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: C; Genetics:
                                                                                                                           A;Gene: attD
                                                                                                                                                         A;Cross-references: GB
A;Experimental source:
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                                                                                                                                                                                                 A; Molecule type: DNA
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A; Residues: 1-84 <STO>
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                                                       Matches
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                           2 VPGSQ 6
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                                                                                                             plasmid
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                                                       Similarity
5; Conserv
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3; Conser
94
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                                                       Conservative
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                                                                                                                                                         :AE008687; I
strain C58
                                                                  66.7%;
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Pred. No. 2e+0
3; Mismatches
                                                       0;
                                                                                                                                                         PIDN:AAL45820.1;
8 (Dupont)
                                                                     Score 26;
Pred. No.
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                          11-Jan-2002 #text_change 11-Jan-2002
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2e+02;
                                                       DB 2; Le
2.3e+02;
hes 0;
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                                                                                                                                                                      PID:g17743559;
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                                                                                 Length 96;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                 T.; Levy,
                                                                                                                                                                                                                                                                                                                                                Wood, G.E.;
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                                                                                                                                                                      GSPDB:GN00188
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myelin basic protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 21-Oct-1992 #sequence_revision 21-Oct-
C;Accession: A6022
R;Aruga, J.; Okano, H.; Mikoshiba, K.
J. Neurochem. 56, 1222-1226, 1991
A;Title: Identification of the new isoforms of A;Reference number: A60222; MUID:91162193
A;Accession: A60222
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-20 <YAN>
C; Superfamily: phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              notechis II-5b nontoxic venom protein - common tiger snake (fragment)
C;Species: Notechis scutatus scutatus (common tiger snake, mainland tiger snake)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
C;Accession: A39328
R;Yang, C.C.; Chang, L.S.; Wu, F.S.
Toxicon 29, 1337-1344, 1991
A;Reference number: A39328; MUID:92263371
A;Accession: A39328; MUID:92263371
A;Accession: A39328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical 11.4K protein (moth 3' region) - phage T4
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 08-Oct-1999
C:Accession: JV0104
R:Uzan, M.: Brody, E.; Favre, R.
Mol. Microbiol. 4, 1487-1496, 1990
A:Reference number: JV0101; MUID:91141300
A:Accession: JV0104
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JV0104
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A;Gene: mot
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A; Residues: 1-99 <UZA>
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Best Local S
Matches 4
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Best Local S
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mes 3; Conserv
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80.0%;
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Pred. !
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Pred. No.
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Pred. No. 2.3e+02;
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ed. No. 2.3e+02;
Mismatches 0;
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                                                                                                                      21-Oct-1992 #text_change
                                                                                                                                                                                                                                                                                                                            25;
No.
                                                     of mouse myelin basic protein: the existence
                                                                                                                                                                                                                                                                                                            0;
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Search completed: October 24, 2002, 15:37:41 Job time: 8.27869 secs

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Listing first 45 summaries
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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39
1 EVPGSQH 7
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Y13E_BPT4
GON1_CHICK
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RLX_HALMA
EA57_HUMAN
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LCRS_YENG
LCRS_YENG
YAFL_DROPS
Z600_DROME
EM6_ARATH
PPK6_PERAM
GRP_CANFA
CBBA_NITVU
PKM_SCYCA
TAT_HV1B5
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R14A_MYCTU
RS14_MYCLE
R135_CHLPN
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HPIS_THIPF
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P20057 gallus gall
P14125 haloarcula
043247 homo sapien
P30816 simian herp
Q29011 sus scrofa
P32280 bacteriopha
Q29031 yersinia pe
P52001 mycobacteri
Q44091 drosophila
Q20973 arabidopsis
P82693 periplaneta
P02999 canis famil
P37102 nitrobacter
P35491 scyliorhinu
P04612 human immun
P04612 human immun
P09165 aeromonas s
P95065 mycobacteri
Q3296 mycobacteri
Q3296 mycobacteri
Q3296 mycobacteri
Q32618 chlamydia p
Q84848 mesobuthus
P01487 leiurus qui
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P00263 thiocapsa p
P34075 boulengerin
P52586 orf virus (
P52587 orf virus (
P78415 homo sapien
O61835 mus musculu
O97797 sus scrofa
P39499 bacteriopha
P37042 gallus gall
P20057 gallus gall
P14125 haloarcula
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STANDARD;		69.2% 71.4% ative	10036	831; HIV_Tat. at; 1. HIVTATDOMAIN gulation; Act		is statement is not remove s a license agreement (Se to license@isb-sib.ch).	Institu ormatic	ATION:	CYCLIN	CRIPTIC G RESPO	son S., y of th m Afric	PubMed=2	ncy virus ruses; Re	05, Created 05, Last se 40, Last ar activating	DARD;		72 1 75 1 75 1 79 1 81 1 83 1 84 1	9974
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P34075;
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01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
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 PIR;
                                                TOXICON 29:1315-1327(1991).
-I- FUNCTION: PRODUCES PERIPHERAL PARALYSIS
TRANSMISSION AT THE POSTSYNAPTIC SITE. I
                                                                                                         water cobras, christyi.";
                                                                                                                                                                                                                                                        Lepidosauria; Squamata;
Elapidae; Bungarinae; Bc
NCBI_TaxID-8610;
                                                                                                                                                                                                                                                                       Boulengerina annulata annulata (Banded water cobra).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Lepidose; Bungarinae; Boulengerina.
                                                                                                                           WEDLINE=92263369; PubMed-1814007; Weinstein S.A., Schmidt J.J., Smith L.A. "Lethal toxins and cross-neutralization water cobras, Boulengerina annulata annu
                                                                                                                                                                                                      TISSUE-Venom;
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Short neurotoxin
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 MISCELLANEOUS: A39327; A39327
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Proteobacteria;
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protein (HiPIP).
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IRON-SULFUR (4FE-4S)
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                                                                                                                                                                 Smith L.A.;
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VF09_ORFN2
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DISULFID 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Lyttle D.J., Fraser K.M., Fleming
"Homologs of vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   poxvirus orf virus.";
J. Virol. 68:84-92(1994)
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PROSITE; PS00272; SNAKE_TOXIN;
                                                                                                                    VF09_ORFN7
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Pro; IPR003571; Snake_toxin.
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                  homolog
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23 BY SIMILARITY.
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59 BY SIMILARITY.
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no RNA stage; Poxviridae; Chordopoxvirinae;
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growth factor are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update]
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                         DNA_BIND
                                                                                                                                                                                 MIM;
                                                                                                                                                                                                                                        modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis M.T., Strickland P.A., ROSS S., Snyder C.J., Danie "IRX: a new family of human homeobox genes from the brea Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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MEDLINE=94076465; PubMed=8254780;
LYTTLE D.J., Fraser K.M., Fleming S.B., M
"Homologs of vascular endothelial growth
poxvirus orf virus.";
J. Virol. 68:84-92(1994).
-!- SIMILARITY: TO VAC ORF PROTEIN F9.
                                                                                                                                                                                                   EMBL; U90308; AAB50006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
                                                                                                            PROSITE;
                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Creat
15-JUL-1998 (Rel. 36, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P78415;
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Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
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                                                                                                                                                                                 606197;
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                                                                                                         PS50071; HOMEOBOX_1;
                                                                    DNA-binding;
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                      37
86
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annotation update)
protein IRX-1 (Fragment)
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1; Mi
21C263AE9450D7B6 CRC64
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                                       HOMEOBOX (TALE-TYPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                PARTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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RESULT 7

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Best Local
                                                                        MGD; MGI:107497; Fxyd3.
Interpro; IPR000272; ATP1GI_PLM
Pfam; PF02038; ATP1GI_PLM_MAT8;
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Ionic ch
                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mat-8, a novel phospholemman-like protein expressed in human tumors, induces a chloride conductance in xenopus oocytes.";
J. Biol. Chem. 270:2176-2182(1995).
-i- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE WHEN EXPRESSED IN XENOPUS OOCYTES. MAY BE A MODULATOR CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison B.W., Leder P.; "neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 3 precursor (Chloride conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein)
(Phospholemman-like).
                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Breast;
MEDLINE=95060797; PubMed=7970700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morrison B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSION.
MEDLINE=95138184; PubMed=7836447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Breast tumor;
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                                                      SIGNAL
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                                                                                                                                                                                                                               X93038; CAA63606.1; -.
                                                                                                                                                                                                       BC002039; AAH02039.1;
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                                                      channel; Ion POTENTIAL.
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Pred. No. 2.3e+02;
                         FXYD DOMAIN-CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; | Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                      "Structures of P-type transporting ATPases and chromosomal locations of their genes.";
of their genes.";
Cell Struct. Funct. 23:315-323(1998).
i- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHICARIDE CHIRAPANT
                                                                                                                                                                                    EMBL; AB015759; BAA35078.1; -.
InterPro; IPR00272; ATP1G1_PLM_MAT8.
Pfam; PF02038; ATP1G1_PLM_MAT8; 1.
PROSITE; PS01310; FXYD; 1.
                                                                                                                                                                                                                                           modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
FXYD domain-containing ion transport regulator 3 |
FXYD domain-containing ion transport regulator 3 |
FXYD domain-containing ion transport regulator 3 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                          SEQUENCE
                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Futai M., Sato R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99140476; PubMed=10206733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
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82
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Struct. Funct. 23:315-323(1998).

FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE CURRENT
FUNCTION: INDUCES A HYPERPOLARIZATION BE A MODULATOR CAPABLE OF
                                                                                                                                                                                                                                                                                                                                       WHEN EXPRESSED IN XENOPUS OCCYTES. MAY BE A MODULATOR CAPA ACTIVATING ENDOGENOUS OCCYTE CHANNELS. SUBCELLULAR LOCATION: Type I membrane protein (Potential). SIMILARITY: BELONGS TO THE FXYD FAMILY.
                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long
          PGSQH 7
PGSAH
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                                                      Similarity
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                                                                                                      CYTOPLASMIC
                                                                                                                EXTRACELLULAR POTENTIAL.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
9CD61684B856E35D CRC64;
                                           Mismatches
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                                                                Length 88
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r 8 kDa protein).
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Sus.
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Y13F_BPT4
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Best Local S
Matches 4
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01-FEB-1991 (Rel. 17, Createw,
01-JUN-1994 (Rel. 29, Last sequence update,
01-JUN-1994 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
Progonadoliberin I precursor [Contains: Gonadotropin releasing
'""+*inizing hormone releasing hormone I) (Gonadotropin releasing
'""+*inizing hormone releasing hormone I); GRH-associated peptide I).
                                                                                                                        STARIN-WHILL
STARIN-WHILL
MEDLINE-94059355; Pubrace
Munn I.C., Chen Y., Hook C., Shar
Dunn I.C., Trization of the chicken
                                                                                                  J. Mol.
[2]
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P39499;
01-FEB-1995
01-FEB-1995
01-MAR-2002
        SEQUENCE OF 24-33.
TISSUE-Hypothalamus;
TISSUE-Hypothalamus;
MEDLINE-82265778; PubMed=7050119;
King J.A., Millar R.P.;
"Structure of chicken hypothalamic luteinizing hormone. II. Isolation and characterization.";
J. Biol. Chem. 257:10729-10732(1982).
                                                                                                                                                                                                                                                                                                                                                                    GON1_CHICK
P37042; P20407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.

Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;

"Bacteriophage T4 genome analysis.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 91
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T4-like phages.
NCBI_TaxID=10665;
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Y13F OR CD.3.
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                                                                                                                 Endocrinol.
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31,
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Veognathae; Galliformes; Phasianidae;
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preprogonadotrophin-releasing
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P20057;
01-FEB-1991
01-FEB-1991
01-NOV-1997
     Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone. I. Structural determination on partial material.";
                                                        MEDLINE-88339942; PubMed-3421961; Wellner D:, Cheng K.C., Mueller-Eberhard "N-terminal amino acid sequences of the |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
PEPTIDE
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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King J.A., Millar R.P.;
"Structure of avian hypothalamic gonadotrophin-releasing hormone.";
S. Afr. J. Sci. 78:124-125(1982).
                                        and
                                                                                                                                                                                                                                Gallus
                                                                                                                                                                                                                                                                                                                                                                                  CHICK
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PIR; S33507; S33507.
InterPro; IPR002012; GnRH
InterPro; IPR004079; Gonac
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-!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS
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MEDLINE=82265777; Pubb.
King J.A., Millar R.P.
                                                                                                                    SEQUENCE
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-!- SIMILARITY: BELONGS TO THE GNRH FAMILY
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                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                   Hemopexin
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   chem. Biophys. ReFUNCTION: BINDS
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GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I.
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AMIDATION (G-34 PROVIDE AMIDE G
AMIDATION (G-34 PROVIDE AMIDE G
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; Galliformes; Phasianidae; Phasiani
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Dr 30-MAY-2000 (Rel. 39, Last sequence update)
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Dr 30-MAY-2000 (Rel. 39, Last annotation update)
Dr 30-MAY-2000 (Rel. 39, Last annotation update)
Dr 30-MAY-2000 (Rel. 39, Last annotation update)
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16-OCT-2001
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                                                           Eukaryota; Metazoa; 
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE LX:
PIR; SO6848; RSHS32.
InterPro; IPR002768; Ribosomal_LX.
Pfam; PF01911; Ribosomal_LX; 1.
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Archaea; Euryarchaeota;
NCBI_TaxID=2238;
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PROSITE; PS00024; HEMOPEXIN; PARTIAL.
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                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                Simian herpes B virus (Cercopithecid herpesvirus 1) (Shbv). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus. NCBI_TaxID=10325;
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                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                    Killeen A.M., Harrington L., Wall L.V.M., Kelly D.C.; "Nucleotide sequence analysis of a homologue of herpes simplex virus type 1 gene US9 found in the genome of simian herpes B virus."; J. Gen. Virol. 73:195-199(1992).
                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein
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n E homolog (Fragment).
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RESULT 15
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-i- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACTION OF THIS PROTEOGLYCAN IS A MAJOR FUNCTION OF THIS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY THE STORES AND AN AMINO-TERMINAL GLOBULAR REGION. MREGULATORY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
                                                                                                                                                                                                                                            InterPro; IPR000538; Link.
InterPro; IPR001304; lectin_c.
PR0SITE; PS01241; LINK; PARTIAL.
PR0SITE; PS00615; C_TYPE_LECTIN__;
PR0SITE; PS50041; C_TYPE_LECTIN__2;
                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cartilage;
MEDLINE=95128522; PubMed=7827755;
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Mammalia;
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Q9M4H3
Q9RJ49
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148.629 Million cell updates/sec
         O9fqi8 amaranthus
O9fqj8 amaranthus
O99fqj8 amaranthus
O99fqj8 yritis vinif
O9rj49 streptomyce
O95146 homo sapien
O99816 agaricus bi
O29241 sus scrofa
O96tc5 homo sapien
O91116 human metap
O98401 rhizobium
O971288 drosophila
O77288 drosophila
O9bu94 homo sapien
O915962 homo sapien
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O915963 homo sapien
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Q9vqw3 drosophila		83	64.1	25	*
Q9zts5 zea mays (m		80	64.1	25	ω
Q9xxe2 caenorhabdi		76	64.1	25	N
	2	70	64.1	25	
Q98pd5 rhizobium l	16	67	64.1	25	0
Q09070 rattus norv	11	67	64.1	25	φ
Q16505 homo sapien	40	64	64.1	25	æ
Q9z9s3 bacillus ha	2 0	63	64.1	25	7
Q90wp2 fugu rubrip	13	27	64.1	25	σŋ
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Q902v1 simian t-ce	15	26	64.1	25	42
Q902v2 simian t-ce	15	26	64.1	25	ω
Q37764 mytilus edu	œ	99	66.7	26	N
homo sap	4	97	66.7	26	_
a	20	96	66.7	26	0
Q9caz6 arabidopsis	10	94	66.7	26	Φ
Q9kag3 bacillus ha	16	84	66.7	26	в
Q98428 paramecium	12	84	66.7	26	7
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Q9i6b5 pseudomonas	16	66	66.7	26	+
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Q9tph2 mastacembel	7	63	66.7	26	N
Q9tu82 canis famil	6 Q	51	66.7	26	_
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Q18842 caenorhabdi	υ D	93	69.2	27	Ψ
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O81995 lycopersico		89	69.2	27	7

ALIGNMENTS

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RESULT 2
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Q9FQI8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
REVERSE TRANSCRIPTASE-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                             retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF232993; AAG44333.1;
Interpro; IPR003006; Iq_MHC.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                        Amaranthus quitensis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.
NCBI_TaxID=107609;
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                TRANSPOSON=COPIA-LIKE RETROTRANSPOSON;
                                                                                                                                                                                                                                                                                                   "Reverse transcriptase sequence evolution in copia-like
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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71.4%;
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01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Q9M4H3;
Q9M4H3;
                                                                                                                                                                     "Differential screening indicates a dramatic change in mRNA during grape berry ripening. Cloning and characterization of encoding putative cell wall and stress response proteins."; Plant Physiol. 122:803-812(2000).
EMBL; AJ237990; CAB85630.1; -.
SEQUENCE 65 AA; 6777 MW; B5EA7D8D7B9170D4 CRC64;
                                                                                                                                                                                                                                                                                                         Vitis.
                                                                                                                                                                                                                                                  STRAIN-CV. SHIRAZ; TISSUE-FRUIT; MEDLINE-20177861; PubMed-10712544;
                                                                                                                                                                                                                                                                                                                              Vitis vinifera (Grape).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation updat
PUTATIVE METALLOTHIONEIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eu Caryophyllidae; Caryophyllidae;
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TYEMBLYEL. 16, Created)
01-MAR-2001 (TYEMBLYEL. 16, Last sequence update)
01-JUN-2001 (TYEMBLYEL. 17, Last annotation update)
REVERSE TRANSCRIPTASE-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                         Davies C.,
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Spermatophyta;
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                                                                            III :II
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5; Conser
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                        PRELIMINARY;
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57.1%;
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yta; eudicotyledons; core eudico;
lales; Amaranthaceae; Amaranthus
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                                                                                                                         Score 30; DB Pred. No. 30; 1; Mismatches
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2; Mismatc
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RESULT
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Best Local
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                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99454989; PubMed=10523621;

MEDLINE-99454989; PubMed=10523621;

De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;

De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;

"DNA methylation is the primary silencing mechanism for a "DNA methylation is the primary silencing mechanism for a "DNA methylation is the primary specific genes with a CpG-rich promoter."
                                                                                                                                                                                                                                LAGE-2.
LAGE-2.
Homo sapiens (Human).
-- "arvota; Metazoa; Chordata; "-- "heria; Primates;
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line- and tumor-specific genes with Mol. Cell. Biol. 19:7327-7335(1999).
EMBL; AF038567; AAD05203.1; -.
EMBL; AJ275977; CAB76944.1; -.
SEQUENCE 58 AA; 6188 MW; ED12057
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                      SEQUENCE FROM Lethe B.G.;
                                                                                                                                                   "A Breast and Melanoma-Shared Tumor Antigen: Antigenic Peptides Translated from Different J. Immunol. 161:3596-3606(1998).
                                                                                                                                                                                               SEQUENCE FROM N.A. Wang R.-F., Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 8 Mb Streptomyces coelicolor A3(2) Mol. Microbiol. 21:77-96(1996). EMBL; AL132644; CAB59435.1; -.
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MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                            Submitted
                                                                                                                                                                                     Schwartzentruber D.J., Rosenberg S.A.;
                                                                                                                                                                                                                                                                                                                                          095146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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Thomson N.R.,
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Catarrhini;
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Matches
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"Development of Agaricus bisporus sporoph
detachment is maintained by the expressic
nutritional genes.";
Submitted (JAN-2000) to the EMBL/GenBank,
EMBL; AJ271695; CAB85689.1;
InterPro; IPR002086; Aldehyde_dehydr.
PROSTTE; PS00070; ALDEHYDE_DEHYDR_CYS; UN
                                                                                                                                                                                                                                                                                                                                  Q29241;
Q29241;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           TISSUE=SMALL INTESTINE;
MEDLINE=96327607; PubMed=8672129;
Winteroe A.K., Fredholm M., Davie
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STRAIN=HORST U3;
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                                                         EMBL;
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                                                                                           ibrary.";
                                                                                                            Evaluation and characterization
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                                                       F15070;
                                                                      Genome 7:509-517(1996).
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5; Conservative
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Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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                                                                                                                                                                                                                                        Chordata; Craniata; Vert Cetartiodactyla; Suina;
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71.4%;
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83.3%;
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Last sequence up
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                                                                                                                                 Davies
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Pred.
 49CF21FECABB1613 CRC64;
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Mismatches
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                                                                                                            porcine
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ina; Suidae;
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                                                                                                            small intestine
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Sus.
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RESULT
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Q91L16
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Best Local S
Matches 4
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Best Local S
Matches
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Q96TC5;
Q96TC5;
Q1-DEC-2001 (TrEMBLrel. 19, C)
Q1-DEC-2001 (TrEMBLrel. 19, L)
Q1-DEC-2001 (TrEMBLrel. 19, L)
Q1-DEC-3001 (TrEMBLREL 19, L)
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-99123683; PubMed-9924608;
Yasuda T., Takeshita H., Iida R., T:
Yasuda T., Mori S., Kishi K.;
Nakashima Y., Mori S., Kishi K.;
                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                         MEDLINE=21279106; PubMed=11385510; van den Hoogen B.G., de Jong J.C., Grochter R.A., Osterhaus A.D.; "A newly discovered human pneumovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91L16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=93-1;
                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Metapneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                  with respiratory tract disease."; Nat. Med. 7:719-724(2001).
EMBL; AF371341; AAK62945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Human metapneumovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB008565; BAB55597.1;
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Ann. Hum. Genet.
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                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=162145;
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Similarity 71.5; Conservative
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                                                                          5142 MW;
                  69.2%;
71.4%;
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el. 19, Last sequ
el. 19, Last anno
el (FRAGMENT).
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Score 27; DB Pred. NO. 98; 0; Mismatches
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2; Mismatches
                                                                              15A0DAA7C7C472BF
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65;
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                                      Length 47;
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Best Local S
Matches 4
          Pfam; PI
                                "Genetic and molecular features of Su(P), a gene that in ref(2)P in male fertility of Drosophila melanogaster."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL; AJ011320; CAA09596.1; - HSSP; P23724; 1RYP, FlyBase; FBgn0002284; Pros26.
InterPro; IPR001353; Proteasome.
                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                           077288;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE
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STRAIN-MARF303099;
MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Watanabe A., Idesawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
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01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
                                                                                                                       Boukhatem N., Bichon Contamine D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003013; BAB53699.1;
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                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      PROS26 PROTEIN (FRAGMENT). PROS26 OR CG4097.
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"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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59 AA;
 61
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 ξ.
                       proteasome; 1.
 6706 MW;
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                                                                                                                                    A., Gay P.,
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18,
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Last annotation update)
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Pred. No. 1.2e
1; Mismatches
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 1179A3032EA6486E CRC64;
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                                                                                                                                    Dru P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                    Petitjean A.M.,
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                                                                                                            interacts with
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Q9BU94;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                              Q97C07;
Q97C07;
01-OCT-2001
                                                                                                                    SEQUENCE FROM N.A.

STRAIN-GSS1 / DSM 4299 / JCM 9571;

MEDLINE-20570466; PubMed-11121031;

Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.

Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K.,

Kawashima Ohya Y., Watanabe K., Yamazaki H., Makino K., Suzuki H.

Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILAR TO HIFT-HOMO SAPIENS (Human).
Homo sapiens (Human).
Tharyota; Metazoa; Chordata; Metazoa; Primates;
                                                            SEQUENCE
                                                                                           sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC002811; AAH02811.1;
Hypothetical protein.
SEQUENCE 69 AA; 7649 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (FEB-2001) to the
EMBL; BC002811; AAH02811.1;
                                                                                                                                                                                    NCBI_TaxID=50339;
                                                                                                                                                                                                                                       TVG0307586
                                                                                                                                                                                                                                                            01-OCT-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=PLACENTA, CHORIOCARCINOMA;
                                                                                                                                                                                                                  Thermoplasma volcanium.
Archaea; Euryarchaeota;
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01-OCT-2001 (TrEMBLrel.
LEUCINE-RESPONSIVE REGUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILAR TO HYPOTHETICAL PROTEIN FLJ20378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                'Archaeal adaptation to higher temperatures
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17, Last sequence update)
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Last annotation updat
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O81376;
O81376;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
REVERSE TRANSCRIPTASE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. H722; TISSUE-LEAF;
ROGERS S.A., Pauls K.P.;
"Tyl-copia class retrotransposons of tomato.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF072638; AAC34805.1; ...
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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HSSP; P01233; 1XUL.
InterPro; IPR000359; Cys_knot.
InterPro; IPR001545; Glyco_hormone_beta.
Pfam; PF00007; Cys_knot; 1.
SMART; SM00068; GHB; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
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MEDLINE-93103017; PubMed-8416675;

Peele M.E., Carr F.E., Baker J.R.Jr.,

"TSH beta subunit gene expression in

"TSH beta subunit gene expression in

Am. J. Med. Sci. 305:1-7(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Search completed: October 24, 2002, 15:36:49 Job time: 11.1475 secs

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     AAP30265
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AAR85125
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AAR76748
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                                                                                                                                                                                                                                                                  SUMMARIES
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Cholera toxin B/en Cholera toxin B/en Cholera toxin B/en Cholera toxin B/en CTP3 epitope of th Cholera toxin B an Cholera toxin B/en E. coli heat labil Residues 50-64 of Sequence of amino Network polymer wh
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i LTB	i LTB	۲. ۱	coli LTB protei	era c	era	cholera strain		<	Plant-optimized E.	id seque	Cholera toxin B su	nit of the	LTB			rac	₩				cid seque	toxin B	ra t	la	Synthetic cholera	Sequence of sub-un		la	coli heat-labil	a coli	osyl	ence of amino

ALIGNMENTS

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RESULT 1
AAY87460
                                                                                                                                                                             Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                Williams NA, Hirst TR;
                                                                                   07-SEP-1998;
                                                                                                   07-SEP-1999;
                                                                                                                                    WO200014114-A1.
                                                                                                                                                             Vibrio cholerae
                                                                                                                                                                                                              Cholera toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                03-JUL-2000 (first entry)
                                                                                                                                                                                                                                                  AAY87460;
                                                                                                                                                                                                                                                                 AAY87460 standard; peptide;
                                                                                                                    16-MAR-2000.
                                                                                                                                                    Escherichia coli.
                                                                 (UYBR-) UNIV BRISTOL.
                                                                                   98GB-0019484
                                                                                                    99WO-GB02970.
                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                NO:2
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\rm GM-1}$ -

WPI; 2000-256943/22.

ب.

Page 13; 62pp;

English.

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RESULT 2
AAY87464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are CC composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and Ccross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as CC cormal EtxB and ctxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea.

CC for treating, preventing and/or modulating a disease associated with an accomposition of a composition of a treating and second diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conser
                                                          Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                 glycolipid receptor GM-1
                                                                                                                                                                                                                                                                07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cholera toxin B/enterotoxin B-derived immunomodulatory peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY87464 standard; peptide;
                                                                                                                     WPI; 2000-256943/22.
                                                                                                                                                                                          (UYBR-) UNIV
                                                                                                                                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                    WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lmmune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVPGSQH 7
                                                                                                                                                       Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA;
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                          BRISTOL
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                                                                                                                                                       Hirst TR;
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Pred. No. 6.4
0; Mismatches
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. 6.4e+05;
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                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EtxB;
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Example 5;

Page 45; 62pp; English

Disclosure; Page 15; 62pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The invention relates to peptide fragments of the Escherichia coli heat CC labile enterotoxin (Etx) and its closely related homologue, cholera CC toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are Ccomposed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and Cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention (AAV87461-Y87463) are fragments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the CC same effects as normal EtxB and CtxB subunits, except that they do not CC bind or cross link GM-1. They may be used in medicine as an inhibitor for CC immunomodulator or adjuvant. They may also be used as an inhibitor for CC toxin-induced diarrhoea. Therefore, the peptides may be used in the CC disease associated with an immune disorder and/or toxin-induced corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB and CtxB has immunomodulatory effects. Peptide AAV87464 corresponds to residues CC sandomly selected control peptide. According to a portion of the beta-4-alpha-2 loop, and peptide AAV87465 is a ccardinal selected control peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                               Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor {\tt GM-1} -
                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2000
                                                                                                       WPI; 2000-256943/22.
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                                                                                                                                                                                                                                                                                                                        WO200014114-A1
                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY87461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY87461 standard;
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                                                                                                                                                                           (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       randomly selected control peptide.
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                                                                                                                                          NA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                        Hirst TR;
                                                                                                                                                                                                              98GB-0019484
                                                                                                                                                                                                                                                 99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
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Pred. No. 6.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID
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       This sequence corresponds to the CTP3 epitope of the Cholera toxin subunit. The DNA sequence encoding this ligates to othersynthetic oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immunous control of the control of 
                                                                                                                                                                                                                                                                                                                  New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marjarian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epitope of Cholera toxin B subunit; flagellin fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRAXIS BIOLOGICS INC
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                      fig.4B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stocker
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                                                                                                                                                                                                  137pp;
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which can be used in
                                                                                                                                                                                                  English
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Pred. No. 0.29;
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               for immuno-
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RESULT 5
AAR85125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                             Matches
                                                       Query Match
Best Local :
                                                                                                                        A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and egs. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica c thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                                                     Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                    Claim 7; Page 25; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy
                                                                                          Sequence
                                                                                                                 secretory
                                                                                                                                                                                                                                                                                                    WPI; 1995-403805/51.
                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09529701-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conjugate; cholera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR85125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intestines; antibodies; secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conjugate; cholera; B toxin; peptide fragment; microparticulate; lnert carrier; modified silica; thyroglobulin; oral vaccine; lmmunisation; infection; insoluble; digestive tract; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
EVPGSQH
                        EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVPGSQH 7
                                            Similarity 7; Conserv
                                                                                                                                                                                                                                            silica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                 IgA class.
                                                                                                                                                                                                                                                                                                                           Mirelman D,
                                                                                          15
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                                           100.0%; ilarity 100.0%; Conservative
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                                                                                          ΑĄ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
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                                                                                                                                                                                                                                                                                                                           Sela
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                                             0;
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Pred. No. 0.3
0; Mismatches
                                            Score 39; DE
Pred. No. 0.3
0; Mismatches
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                                                       DB 16;
0.37;
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                                                                   Length 15;
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RESULT 6 AAY87462

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RESULT 7
AAY87463
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Best Local
                                                                                                                                                                                                                                                                                                                                               GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (ETXB and CTXB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and CTX, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of ETXB and/or CTXB, exerting the same effects as normal EtxB and CTXB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to peptide fragments of the Escherichia coli he labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycolipid receptor GM-1 -
   AAY87463;
                                 AAY87463 standard; peptide; 21
                                                                                                                                                                                                                                                                      Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-256943/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams NA, Hirst TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1998;
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000
                                                                                                                                                                                                                                             Sequence
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                                                                                                              1 EVPGSQH 7
|||||||
7 EVPGSQH 13
                                                                                                                                                                             1 Similarity
7; Conserv
                                                                                                                                                                                                                                             21
                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                             AA,
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Pred. No. 0.5
0; Mismatches
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                                                                                                                                                                                                            Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli heat
                                                                                                                                                                              Gaps
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                                                                                                                                                                             0;
RESULT 8
AAR76748
ID AAR7
XX
AC AAR7
XC AAR7
XX
DT 18-M
XX
Resi
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В
                          Qy
                                                                                                                          Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                              GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/Or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant.
                                                                                                                                                  Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y874 represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams NA, Hirst TR;
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycolipid receptor GM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of Escherichia coli heat labile enterotoxins useful immunomodulators and for treating diarrhea and which do not bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile enterotoxin subunit B; EtxB;
beta-4-alpha-2 loop; GM-1 ganglioside receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli heat labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2000
                           1 EVPGSQH 7
EVPGSQH 13
                                                            7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune disorder;
                                                                                                                          21
                                                              Conservative
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                                                                                                                          AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0019484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxin B-derived
                                                                           100.0%;
                                                              0;
                                                                            Score 39; I
Pred. No. 0.
                                                              Mismatches
                                                                                           DB
                                                                            .52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide, SEQ ID NO:5
                                                                                         21;
                                                              0;
                                                                                                                                                       . Sequences AXY87460-Y87463
AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulation;
                                                                                           Length 21;
                                                               Indels
                                                              0
                                                              Gaps
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Residues 50-64 of cholera toxin B subunit and FimH 224-226

18-MAR-1996

(first entry)

AAR76748

AAR76748 standard; Protein; 23 AA

0,

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RESULT 9
AAP30265
ID AAP3
XX
AC AAP3
                                                                                                                          Query Match
Best Local Similarity
"---hes 7; Conserv
                                                                                                                                                                                         В
                                                                                                           Qy
                                                                                                                                                                                                                       of the hepatitis B virus surface antigen pre-52 region into a different position of the FimH adhesin of type I fimbriae. Restiction site handles (BgIII-sites) were introduced into the fimH gene, and the foreign epitopes are then inserted in-frame. In the selected positions the insertion of the epitopes did not significantly alter the adhesive function of the FimH protein. The expression of the chimeric proteins on the surface of fimbriae on bacterial hosts illustrated the possibility of using bacterial adhesins as general presenters of foreign antigens and epitopes. These chimeric genes may be used in the production of variant FimH adhesins which may be useful for targetting active compounds and microbial cells to locations comprising selected receptors to which
                                                                                                                                                                                                                                                                                                                                                                 which was used in the production of fimH fusion genes comprising the cholera toxin B subunit inserted into the fimH gene. This insert shows the inclusion of the B subunit into the FimH protein at position 224-226. The chimeric genes were then opt, further modified by insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FimA;
 AAP30265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor specific bacterial adhesins - compounds and microbial cells to locati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
                          AAP30265 standard;
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a fragment of the the plasmid pLPA93
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GXBI-) GX BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-1995;
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                                                                                      σ
                                                                                                                                                                                                                 adhesins bind
                                                                                    EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klemm P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
Escherichia coli
                                                                                                                                                                                         23
                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-DK00042
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23
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20..22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note=
                        Protein;
                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Represents FimH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ś
                                                                                                                                       0;
                                                                                                                                                Score 39; DB 1
Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pallesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin B
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locations of receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subunit 50-64"
                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sokurenko
                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for targetting
                                                                                                                                                               Length
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EV
                                                                                                                                                               23;
                                                                                                                                      0;
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                   insertion
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Network polymer which comprises a series of composite E. labile toxin (LT)/heat-stable toxin (ST) polypeptide repe

repeating untis

Heat-labile enterotoxin; heat-stable toxin; vaccine; ss

W08502611-A

Synthetic

20-JUN-1985

₽ Ω

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AAP50439
                                                                                                            RESULT 10
                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAB30264, AAB30265, AAB30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coll (enterctoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CNRS )
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of amino carries an Arg at
                                    AAP50439;
                                                                      AAP50439 standard; protein; 41
                                                                                                                                                                                                                                                                                                                                                     a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1983-834645/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guyongruaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera vaccine;
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                                                                                                                                                                EVPGSQH
                                                                                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                   1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raulais D,
                                                                                                                                                                                                                                        Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids 50-75 of the cholera toxin B1 subunit which posns. 67 and 73.
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                                                                                                                                                                                                                                                           Score 39; DB 4
Pred. No. 0.65;
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RESULT 11
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Best Local S
Matches 7
The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interpolypeptide cystine bonds formed between oxidized Cys resid of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu
                                                                                                                     WPI; 1985-159230/26.
                                                                                                                                                                                                                                                                                                                                                    01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
                                                                Claim
                                                                                    New synthetic polypeptide(s) for part of E. couseful for vaccination of mammals against the
                                                                                                                                          Houghten
                                                                                                                                                                                                           12-DEC-1984;
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                                                                                                                                                                                                                                                                                                Heat-labile
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                                                                                                                                                                                                                                                                                                                                                                                              AAP50436 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1984;
                                                                                                                                                                                                                                                                                                                     labile toxin
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7; Conser
                                                                                                                                                                 SCRIPPS
                                                                Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                               enterotoxin; heat-stable toxin; vaccine; ss
                                                                                                                                                                                                                                                                                                                   (LT)/heat-stable toxin (ST)
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A
                                                               100; 120pp; English.
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                                                                                                                                                                 CLINIC RES
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                AA.
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1;
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                                                                                    coli enterotoxin(s ne enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli enterotoxin(s
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                                                                                                                                                                                                                                                                                                                  ce E. coli h
repeating
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RESULT 12
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                                       Query Match
Best Local S
Matches 7
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Best Local
                                                                                                             The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterctoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                                         Cholera toxin B, sub-unit polypeptide(s) as vaccines medicaments - effective against Escherichia coli and cholerae infections, are prepd. by solid phase peptide cholerae infections.
                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                  Milhaud G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae
                                                                                                                                                                                                                      Claim 8;
                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                       Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholera vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant DNA techniques. X9 is Met or X39 is Asn or Tyr and X46 is Tyr or Asn.
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                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP30600 standard;
                                                                                                      vaccine
23
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                                       Local Similarity es 7; Conserv
                    Н
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EVPGSQH
                    EVPGSQH
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                                                                                                                                                                                                                     Page 11; 13pp;
                                                                                                     1-10mg of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 AA;
                                       100.0%; ilarity 100.0%; Conservative (
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Arg at posns.
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29
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                                                                                  Å,
                                                                                                                                                                                                                                                                                                        Delmas A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; E.coli infection;
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Pred. No.
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                                         Mismatches
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1.2;
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See also AAP50439-57.
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Vibrio
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RESULT 13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             active site; E. coli heat labi
Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1993;
31-MAY-1994;
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                                                                                                                                                                                                             AAY41816;
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Escherichia coli
                                             three-dimensional
                                                                   ADP-ribosylating
                                                                                                                 Escherichia
                                                                                                                                                               08-DEC-1999
                                                                                                                                                                                                                                                      AAY41816 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Oomen R, Read
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RJ, Stein
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94US-0251121
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                                             toxin; PT; crystalline pertussis holotoxin; ETA; structure; LT; immunoprotective; infection.
                                                                                                                 verotoxin-l B-subunit.
                                                                                                                                                                                                                                                         peptide;
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ID AAW95226
XX AW95
XX 16-MA
DT 16-MA
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XX Pertu
KW Pertu
KW enzym
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:
(1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read RJ,
Hazes B,
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                                                                                                                               E. coli heat-labile toxin (LT) beta-subunit sequence
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Oomen RP;
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94US-0251121
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pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;

tion; toxin; crystalline; interacting site; mitoger

structural analysis;

heat-labile;

US5856122-A Escherichia coli.

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Search completed: October 24, 2002, 15:20:27 Job time: 13.2459 secs
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                                                                                                                                                                                                                      The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of CC forming a complex with the holotoxin and which molecule is an effector CC toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional CC identified interacting site(s) are modified by x-ray crystallogaphy. The CC identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure CC of PT have functional and/or structural resemblance to other bacterial CC toxins such as diphtheria toxin (PT), Pseudomonas exotoxin A (ETA), the CC heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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24-AUG-1993;
31-MAY-1994;
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 5; 40pp; English.
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Oomen RP, Re
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                                                                                 1 EVPGSQH 7
                                                                EVPGSQH 47
                                                                                                                                                                                               93 AA;
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93US-0110947.
94US-0251121.
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Stein PE;
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Pred. No. 2.4;
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Result
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1: /cgn2_6/ptodata/1,

2: /sgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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DB
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              US-08-292-968-26
US-08-467-974-26
US-08-467-976-26
US-08-467-976-26
US-08-952-337-5
US-08-952-337-6
US-08-952-337-1
US-08-952-337-1
US-09-911-82-21
US-09-911-82-21
US-09-911-82-21
US-09-911-82-21
US-08-952-337-1
US-08-952-337-2
US-08-952-337-1
US-08-952-337-2
US-08-952-337-1
US-09-031-9520-17
US-09-031-9520-17
US-09-031-9520-17
US-09-031-9520-17
US-09-031-9520-17
US-09-031-9520-17
US-09-031-9520-17
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(without alignments)
41.388 Million cell updates/sec
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Sequence
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26, Appl
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26, Appl
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US-08-292-968-26
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Sequence 4, Appli	PCT-US95-11684-4	IJ	1810	76.9	30	14
•	US-08-954-698-48	4	1299	76.9	30	3
Sequence 48, Appl	US-08-674-509B-48	4	1299	76.9	30	12
Sequence 62, Appl	US-08-460-900C-62	4	1299	76.9	30	1
Sequence 3, Appli	US-09-268-140-3	4	1286	76.9	30	ö
Sequence 6, Appli	PCT-US95-13233-6	G	1285	76.9	30	39
Sequence 6, Appli	US-08-954-668-6	4	1285	76.9	30	88
Sequence 6, Appli	US-08-656-055-6	w	1285	76.9	30	37
Sequence 6, Appli	US-08-540-406-6	N	1285	76.9	30	8
Sequence 2, Appli	US-09-027-337-2	Ν	855	76.9	30	š
Sequence 2, Appli	US-08-366-051B-2	Н	805	76.9	30	34
Sequence 2, Appli	US-08-045-806-2	Н	805	76.9	30	ü
Sequence 1, Appli	US-08-714-070A-1	N	775	76.9	30	32
-	5194375-2	6	459	76.9	30	3
Sequence 8, Appli	US-09-058-260-8	4	329	76.9	30	ö
Sequence 8, Appli	US-08-694-078-8	4	329	76.9	30	29
Sequence 8, Appli	US-08-781-802-8	N	329	76.9	30	8

ALIGNMENTS

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NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MODIFICATION NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Canada ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26, AL
5856122
WAT
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                           amino acids
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COCKLE, Stephen A
OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOOSMORE, Sheena
KLEIN, Michel H.
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linear
             single
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Best Local
                                 Matches
                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/292,968
EILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
EILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
APPLICATION NUMBER: US 08/110,947
                                                                                                                                                                                               TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               FILING DATE: 24-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HAZES, BE
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                               TYPE: amino acid STRANDEDNESS: sir
                                                 Local Similarity
                                                                                                                                                                                                                                                                               NAME: STEWART, Michael REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1111111
41 EVPGSQH 47
                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                               LENGTH:
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 1 EVPGSQH
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5965385
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Suite 701, 330 University Avenue
                                                                                                                                                               93 amino acids
                              100.0%;
ilarity 100.0%;
Conservative (
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linear
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                                                                                                                                                                                                                                (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Randy J.
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                              Score 39; DB 2; Length 93; Pred. No. 0.67; Indels
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                                               RESULT 4
US-08-467-976-26
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Best Local Similarity
Thes 7; Conserve
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Sequence 26, Application US/08467976 Patent No. 6018022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,536

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968

FILING DATE: 22-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121

FILING DATE: 31-MAY-1994

PRIOR APPLICATION NUMBER: US 08/251,121

APPLICATION NUMBER: US 08/251,121

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAZES, BATT
TITLE OF INVENTION: MOI
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                41 EVPGSQH 47
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                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: STEWART, Michael REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                              1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLEIN, Michel H. ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOOSMORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        READ, Randy J.
                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                              Score 39; DB 2;
Pred. No. 0.67;
Mismatches 0
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Length 93; ; Indels

0

Gaps

0;

APPLICANT:

Randy J.

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Query Match
Best Local Similarity
7; Conserve
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US-09-082-514-26
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                                                                                                                                                          Sequence 26, Appl. Patent No. 616892
                                                                                                                            GENERAL INFORMATION:
APPLICANT: READ, Randy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/251
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION UMMER: US 08/110
APPLICATION UMMER: US 08/110
FILING DATE: 24-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION UMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NAMBER: US 08/292,968
PRIOR APPLICATION AND ERIOR 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
              APPLICANT: ARMSTRO APPLICANT: HAZES, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                             APPLICANT:
                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                         41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/467,976 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                       1 EVPGSQH 7
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M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVENTION:
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                                                                                                                                                                           Application US/09082514
                                                        STEIN, Penelope E. COCKLE, Stephen A. COMEN, Raymond P. KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sim & McBurney
Suite 701, 330 University Avenue
                             ARMSTRONG, Glen D. HAZES, Bart
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   linear
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100.0%; Pr
MODIFICATION (
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                PERTUSSIS TOXIN
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SOFTWARE: FastSEQ for Window
SEQ ID NO 5
LENGTH: 102
TYPE: PRT
ORGANISM: Vibrio cholerae
US-08-952-337-5
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                                   Query Match
Best Local Similarity
""" Pes 7; Conserv:
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INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                 APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
Sim & McBurney
'' Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
STATE: Ontario
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1 EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: STEWART, Michael I REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                   Conservative
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                                                                 100.0%;
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                                                                  Score 39; DB 3
Pred. No. 0.73;
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Pred. No. 0.67;
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                                                    Mismatches
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                                                                                  DB 3; Length 102;
                                                   Indels
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EVPGSQH

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GENERAL INFORMATION:

APPLICANT: Holmgren, Jan

APPLICANT: Lebens, Michael R.

APPLICANT: Lebens, Michael R.

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

FILE REFERENCE: 3846/0D758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1998-01-05

EARLIER APPLICATION NUMBER: PCT/SE96/00570

EARLIER FILING DATE: 1996-05-02

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER FILING DATE: 1995-05-05

NUMBER OF SEQ ID NOS: 6

CONTEMBER OF SEQ ID NOS: 6
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US-08-472-171-2
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US-08-952-337-6
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US-08-952-337-6
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Patent No.
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SEQ ID NO 6
LENGTH: 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                     COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
US 08/393,334
                                                                                       APPLICATION NUMBER: US 08 FILING DATE: 23-FEB-1995 ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: 1
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/472,171 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Toronto
STATE: Ontario
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; MOLECULE TYPE: US-08-894-526-2
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GENERAL INFORMATION:
                                                        Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local S
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/894
FILING DATE: 01-DEC-1997
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                            1 EVPGSQH 7
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EVPGSQH 57
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Zealey, Gavin R
Klein, Michel H
                                                           Conservative
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h Floor, 330 University Avenue
                                                                                                                                  protein
                                                                      100.0%;
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                                                                      Score 39; I
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Pred. No. 0.74;
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                                                                        DB 2;
0.74;
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RESULT 10 US-09-013-047-2

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RESULT 11
US-09-374-597-2
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                    Sequence 2, Application US/09374597 Patent No. 6140082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09013047 Patent No. 5998168
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICATION UMBER: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/3
FILING DATE: 23-FEB-1995
ATTORNEY/ACENT INFORMATION:
STANDARY ACENT, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/472,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                          APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
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                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                      NUMBER OF SEQUENCES:
                                                                     TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                      51 EVPGSQH 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I. REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 7; Conserva
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                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                         1 EVPGSQH 7
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M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toronto
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330 University Avenue, 6th Floor
330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                   Sim & McBurney
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 103;
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Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 249
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                          ATTORNEY/AGENT INFORMATION:
                                                                                              CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
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TELEPHONE: 416-595-1155
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. H. TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
TELEX: 065-24567 DI NO: 2:
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CLASSIFICATION:
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ZIP: 77010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/374,597
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                                                  FILING DATE:
                                                                FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/8
                                                                                                                                               FILING DATE:
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                         CITY:
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1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                      USA
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FEBRUARY 23, 1995
                                                  04-AUG-1997
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Pred. No. 0.
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0.74;
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RESULT 14
US-08-952-337-1
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Best Local Similarity
The 7; Conservat
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PCT-US95-13376-21
                                                                                                                               Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/328

FILING DATE: 24-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jones, John W.

REGISTRATION NUMBER: 31,380

REGISTRATION NUMBER: 3617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                51 EVPGSQH
                                                                                                                               Local Similarity
les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/13376
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Pred. No. 0.74;
); Mismatches
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Search completed: October 24, Job time: 6.13115 secs
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                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 123
                                                                                                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
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PATENT NO. 6019973

GENERAL INFORMATION:

APPLICANT: HOLMGren, Jan

APPLICANT: Lebens, Michael R.

APPLICANT: Lebens, Michael R.

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1995-05-05
EARLIER FILING DATE: 1995-05-05
UMBER OF SEQ ID NOS: 6
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CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
FILE REFERENCE: 3846/0D758
                                                                                                                                                                                                                                          LENGTH: 123
TYPE: PRT
ORGANISM: Eschcerichia coli
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is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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Copyright (c) 1993 - 2002 Compus
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US-10-110-364-13
US-10-110-364-13
US-10-110-364-12
US-09-791-537-99772
US-09-791-537-73608
US-09-791-537-73608
US-10-110-364-12
US-09-791-537-28360
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US-09-791-537-36823
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US-09-791-537-368640
US-09-791-537-786640
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US-09-791-537-74385
US-10-110-364-8
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US-09-791-537-38611
US-09-791-537-38639
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                              Sequence 19387, A
Sequence 38611, A
Sequence 38639, A
Sequence 68591, A
Sequence 74385, A
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 36620, A
Sequence 36620, A
Sequence 36620, A
Sequence 20, Appl
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Sequence 4, Appl Sequence 9, Appl	Sequence 123948,	Sequence 5, Appli	Sequence 129309,	Sequence 47818,	Sequence 7, Appl	Sequence 42610,	Sequence 2, Appli	Sequence 130348,	Sequence 131854,	Sequence 15, App	Sequence 23, App	Sequence 21, App	Sequence 19, App	Sequence 18, App	Sequence 16, Appl	Sequence 11, App	Sequence 6, Appl

ALIGNMENTS

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 19387
US-09-791-537-19387
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US-09-791-537-19387
; Sequence 19387, Application US/09791537
; GENERAL INFORMATION:
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; ORGANISM: pdb 1CHPD
US-09-791-537-38611
                                       APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Descent Three Dimensional Structures of Protein Families and Family Me
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 38611
LEMGTH: 103
TYPE: PRT
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RESULT 4
US-09-791-537-68591
US-09-791-537-68591, Application US/09791537
GENERAL INFORMATION:
US-09-791-537-74385
Sequence 74385, Application US/09791537; GENERAL INFORMATION:
APPLICANY: Bionomix, Inc.
APPLICANY: Debe, Derek
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; Sequence 38639, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
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US-09-791-537-38639
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Best Local Similarity
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 68891
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APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 38639
LENGTH: 103
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Matches
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TYPE: PRT
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Pred. No. 2.9;
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SEQ ID NO 8
LENGTH: 103
TYPE: PRT
ORGANISM: Vibrio cholera
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(103)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 998409
US-10-110-364-8
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Best Local Similarity
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Sequence 10, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hadaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBEO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT APPLICATION NUMBER: PCT/US00/27607
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 74385
LENGTH: 103
TYPE: PRT
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                      51 EVPGSQH 57
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US-10-110-364-22
US-10-110-364-22
Sequence 22, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:

NAME/KEY: VARIANT

; LOCATION: (1)...(103)

; OTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235

; OTHER INFORMATION: (Ogawa 41 R35D).
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NAME/KEY: VARIANT

LOCATION: (1)...(103)

OTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511

US-10-110-364-10
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US-10-110-364-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A CURRENT APPLICATION NUMBER: US/10/110,364 CURRENT FILING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05
CURRENT APPLICATION NUMBER: US/10/110,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
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PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 103
TYPE: PRT
ORGANISM: Vibrio cholera
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ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                         51 EVPGSQH 57
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nes 7; Conserv
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Pred. No. 2.9;
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Pred. No. 2
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RESULT 11
US-09-791-537-99772
; Sequence 99772, Application
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 99772
LENGTH: 104
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US-09-791-537-87980
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US-09-791-537-87980
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Best Local S
Matches 7
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Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 87980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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LENGTH: 103
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PRIOR APPLICATION NUMBER: PCT/US00/27607
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TYPE: PRT
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NAME/KEY: VARIANT
LOCATION: (1)...(103)
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Local Similarity 100.0%;
nes 7; Conservative 0
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Pred. No. 2.9;
0; Mismatches
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Pred. No.
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ORGANISM: pdb 3CHBD

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; ORGANISM: pdb 1LTRD US-09-791-537-73608
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US-10-110-364-12
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Best Local S
Matches 7
                Best Local Similarity Matches 7; Conserv
                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 73608 LENGTH: 113
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APPLICANT: Handley, Harold H.
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Best Local :
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                                                                                                                                                                                                                                    APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION UNMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                    APPLICANT: Bionomix, Inc. APPLICANT: Debe, Derek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT LOCATION: (1)...(105) CTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa OTHER INFORMATION: 41).
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TYPE: PRT
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                    Conservative
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                                  100.0%; Score 39; DB 5; Length 113; 100.0%; Pred. No. 3.3;
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                    0;
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                  Mismatches
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                  0;
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Query Match
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; FEATURE:
, NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB
US-10-110-364-20
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Best Local Similarity
Thehes 7; Conserv
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 123
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Haddley, Harold H.
APPLICANT: Hadparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTER
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                              ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(123)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1395122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
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h 100.0%; Score 39; DB 6; Length 123; Similarity 100.0%; Pred. No. 3.6; 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                     variant from
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                                                                                                                     NCBI gene bank GI: 223254
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Gaps

Qy 1 EVPGSQH 7
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Db 71 EVPGSQH 77

Search completed: October 24, 2002, 15:33:19
Job time: 16.8361 secs

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GenCore version 5.1.3
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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(S)-2-hydroxy-acid
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apolipoprotein A-I
apolipoprotein A-I
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interleukin-7 rece
hypothetical protein
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glucarate dehydrat
glutamate synthase
zK112.1 protein -
hypothetical prote
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protein F20B17.2 (
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gibberellin 20-oxi
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5	44	43	42	41	40	39	3 8	37	36	35	34	ω	32	31	30	
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	
76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	
440	436	431	412	376	375	373	336	304	298	291	270	262	182	153	148	
N	Ŋ	N	ν	_	N	2	N	N	N	Ŋ	N	N	N	N	N	
T44138	в70321	A89761	T47142	S17246	T35015	T47115	A72247	F84169	B34791	AI2241	D83072	C34791	D83638	T31701	в72782	
hypothetical prote	flavocytochrome C	hypothetical prote	hypothetical prote	chorismate synthas	probable 3-oxoadip	probable 4-carboxy	DNA-directed RNA p	hypothetical prote	interleukin-7 rece	hypothetical prote	conserved hypothet	interleukin-7 rece	conserved hypothet	hypothetical prote	hypothetical prote	

ALIGNMENTS

A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-20, '0', 22-31, '0', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <shi> A; Experimental source: classical biotype strain 569B R; Dams, E.; de Wolf, M.; Dierick, W. Biochim. Biophys. Acta 1090, 139-141, 1991 A; Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A; Reference number: S17665; MUID:91355224</shi>	A; Residues: 1-124 <hei> A; Cross-references: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94613.1; GSPDB:GN A; Experimental source: serogroup O1; strain N16961; blotype E1 Tor R; Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J. Chinese Biochem. J. 9, 395-399, 1993 A; Title: Nucleotide sequence analysis of the gene encoding the classical biotype V.ch A; Reference number: JC1078 A; Accession: JC1078</hei>	A; Rocicule type: DNA A; Residues: 1-124 < LEW> A; Residues: 1-124 < LEW> A; Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A; Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A; Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A; Heidelberg, J.F; Elsen, J.A; NeC.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Empolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833 A; Ratus: preliminary A; Molecule type: DNA	A; Cross references: EMBL:X36/86; NID:g48420; PIDN:CAA41393.1; PID:g48422 A; Experimental source: strain 2125 R; Lebens, M.; Holmgren, J. submitted to the EMBL Data Library, November 1993 A; Description: Structure and arrangement of the Cholera toxin genes in vibrio Cholera A; Reference number: S39238 A; Accession: S39238 A; Accession: S39238 A; Molecule type: DNA A; Residues: 1-124 < LEB> A; Cross-references: EMBL:X76390; NID:g433856; PIDN:CAA53973.1; PID:g433857 A; Accession: S39241	RESULT 1 XVVCB cholera enterotoxin, B chain precursor VC1456 [validated] - Vibrio cholerae (strain N N,Alternate names: enterotoxin beta chain C;Species: Vibrio cholerae C;Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 C;Accession: S14624; S39238; S39241; H82196; JC1078; S17666; PC1010; A05130; A01819; R;Dams, E.; de Wolf, M.; Dierick, W. R;Dams, E.; de Wolf, M.; Dierick, W. R;Damitted to the EMBL Data Library, March 1991 A;Description: Correction of the cholera toxin nucleotide sequence of the Vibrio chol A;Reference number: S14623 A;Molecule type: DNA A;Residues: 1-124 <dam></dam>

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A; Note: Asn-65 v
C; Comment: The a
C; Genetics:
A; Gene: VC1456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
C;Complex: the cholera enterotoxin molecule contains
C;Complex: the with the subunit B, an aggregate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 22-38,'H','40-42,'N',44-67,'T',69-90,'N',92-124
A; Experimental source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to Asp
C; Comment: The authors translated the codon TCA for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',R;Takao, T.; Watanabe, H.; Shimonishi, Y.
Eur. J. Biochem. 146, 503-508, 1985
Eur. J. Biochem. 146, 503-508, 1985
A;Title: Facile identification of protein sequences by mass spectrometry.
A;Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69,'E',71-90,'N',92-124 <LAI>A; Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69,'E',71-90,'N',92-124 <LAI>A; Note: the difference at residue 70 may be due to deamidation during p: R; Nakashima, Y; Napiorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett 68, 275-278, 1976
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A;Accession: A38033
A;MOlecula +---
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A; Residues: 1-32,'s',34-74,'s',76-124 <MEK>
A; Residues: 1-32,'s',34-74,'s',76-124 <MEK>
A; Cross-references: GB:X00171; NID:948347; PID
R; Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain
A; Reference number: A01819; MUID:78005537
A; Accession: A01819
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-38,'H',40-67,'T',69-124 <DA2>
A;Cross-references: EMBL:X58785; NID:948888;
R;Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. Sci. Sin. B Chem. Biol. Med. Earth Sci. Sci. Sin. B Chem. Biol. Med. Earth Sci. Sci. Sin. B Chem. Biol. Med. Earth Sci. Sin. B Chem. Biol. Med. Biol. Med. Earth Sci. Sin. B Chem. Biol. Med. Biol. Med. Earth Sci. Sin. B Chem. Biol. Med. B
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R; Mekalanos, J.J.; Swartz, D.J.; Pearson,
Nature 306, 551-557, 1983
A; Reference number: A93320; MUID:84068199
RESULT 2
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A; Residues: 22-38, 'H', 40-42, 'N', 44-67, 'T', 69-90, 'N'
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A; Accession: PC1010
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                                                                                                                                                                                                                                                                                                                                                                                                ;Reywords: enterotoxin; toxin
;1-21/Domain: signal sequence #status predicted <SIG>
;2-124/Product: cholera enterotoxin chain B #status
;30-107/Disulfide bonds: #status experimental
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Best Local
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                                                                                                                                                                                    EVPGSQH 7
                                                                                                               EVPGSQH
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A; Molecule type: DNA
A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <YAM>
A; Ricians: 1-27, 'E', 29-63, 'K', 65-124 <YAM>
A; Leong, J.; Vinal, A.C.; Dallas, W.S.
R; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
A; Title: Nucleotide sequence comparison between
A; Reference number: I41194; MUID:85156481
A; Accession: I41194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross references: GB:M17101; NID:g146375; PIDN:AAA23973.1; R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A. FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from A;Reference number: 153542; MUID:93252225
A;Accession: 167644
δÃ
                                                                                                                                                             F;1-21/Domain: signal sequence #status predicted F;22-124/Product: heat-labile enterotoxin chain I
                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A unique amino acid sequence of the B A;Reference number: A61475; MUID:89180953 A;Accession: A61475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-17, (C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A;Residues: 1-17, (C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A;Cross-references: GB:S60731; NID:g408994; PIDN:AAC60441.1; PID:g408996
A;Tsujl, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.
Microb. Pathog. 2, 381-390, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-5,'F',7-17,'C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122
A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831
A; Experimental source: plasmid ENT-R PCG86
R; Ibrahimi, I.; Gentz, R.
J. Biol. Chem. 262, 10189-10194, 1987
                                                                                                                                                                                                                                                          A; Description: the biological activity of the
                                                                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                                                                        C; Complex: the heat-labile enterotoxin molecule
                                                                                                                                                                                                                                                                                                                           A; Experimental
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A; Residues: 1-22 < RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Evolutionary origin of pathogenic A;Reference number: A26946; MUID:87137303 A;Accession: B26946
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R;Yamamoto,
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                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change
;Accession: A01820; B26946; I41194; I41287; I67644; A61475
                                                                                                                                            30-107/Disulfide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A01820
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Bacteriol. 169, 1352-1357, 1987
  1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                        type: protein
22-24,'S',26-27,'E',29-63,'K',65-66,'A',68-95,'A',97-122,
tal source: strain 240-3
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gibberellin 20-oxidase - common N; Alternate names: Ntc16 protein C; Species: Nicotiana + hharm
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A; Note:
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R;Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G96017
                                                                                                                                                                                                                                                                                   RESULT
G96017
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A;Description: Over-expression of a tobacco homeobox gene, NTH15, A;Reference number: Z14418
A;Accession: T01751
                                                                                                                                                                                                               C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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                      A; Molecule type: DNA
A; Residues: 1-137 < KUR>
                                                                                                                                                                                                                                     conserved hypothetical exported protein SMb20700 [imported] - Sinorhizobium meliloti C; Species: Sinorhizobium meliloti
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A;Cross-references: GB:AL591985; PIDN:CAC49807.1; PID:g15141295; GSPDB:GN00167
                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-367 <TAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-272 <WAM>
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A; Accession: T14755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AB016084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: fetal brain; clone DKFZp564A0122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Species: Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          EVPSSQH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   common tobacco
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Pred. No.
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Pred.
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanla, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Seklguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69783
                                                                                                                                                                                                        C;Superfam11
C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain 1021, megaplasmid pSymB R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; ¿ pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
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A; Experimental source: strain 1
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucarate dehydratase (EC 4.2.1.40) - Bacillus subtilis C:Species: Bacillus subtilis
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A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                A;Gene: ycbF
                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-455 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                    Superfamily: glucarate dehydratase
                                                                                                     Matches
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nes 6; Conserv
                                                                                                                                 Local
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                                                                                                   l Similarity
5; Conserv
                                                                                                                                                                                                              carbon-oxygen
                                                                                                     Conservative
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  70
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85.7%;
                                                                                                                              82.18;
71.48;
                                                                                                                                                                                                           lyase;
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Pred. No. 17;
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Pred. No.
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S.; Federspiel, N.A.; Fisher, R.
                                                                                                                                                                                                                                                                                                                                                                                                                            translation
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glutamate synthase (NADPH) (EC 1.4.1.13) small chain C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #t C;Accession: AG0432 R;Patkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R R;Patkhill, J; Wren, B.W.; Thomson, N.R.;

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.;

, R.W.; I Davies,

Holden, M.T.G.; , R.M.; Davis, P.

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#text_change 27-Nov-2001

[imported] - Yersinia pestis

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RESULT 7 AG0432

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il, M.; Rutherford, K.; Sin
Nature 413, 523-527, 2001
A; Title: Genome sequence of
A; Reference number: AB0001;
A; Accession: AG0432
A; Actatus: preliminary
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                                                                                                             A;Molecule type: DNA
A;Residues: 1-137 <BOO>
A;Cross-references: GB:M19058; NID:g149919; PIDN:AAA88230.1; PID:g1196505
C;Superfamily: Mycobacterium leprae hypothetical 15.2K protein
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                                                                                                                                                                                     A; Reference number: A; Accession: B27586
                                                                                                                                                                                                   A;Title: Antigenic proteins of Mycobacterium leprae. Complete sequence A;Reference number: A92821; MUID:88088878
                                                                                                                                                                                                                                                                                   hypothetical protein - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 26-May-2000
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C; Superfamily:
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A;Molecule type: DNA
A;Residues: 1-534 <DUZ>
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A;Description: Sequence of the C. elegans cosmid ZK112.
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C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44886
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C; Keywords: oxidoreductase
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A; Residues: 1-472 <KUR>
A; Cross-references: GB:AL590842;
C; Genetics:
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2 VPGSQH
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Caenorhabditis elegans ZK688.6 protein
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71.48;
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57.1%;
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A; Map po
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protein F20B17.2 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96B27 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: C96B27
                                                          homeobox protein (clone NvHBox-4) - eastern newt
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
                    C;Accession: B48820 R;Beauchemin, M.; Sa
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain A3(2) C; Genetics:
A; Gene: SCOEDB: SC2A11.21c
                                                                                                                                                 RESULT 12
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A; Cross-references: EMB
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A; Accession: T34767
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Best Local
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Gene: SCOEDB:SC2All.21c
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154,
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5; Conserv
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  55-65,
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Savard, P.
5-65, 1992
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71.4%;
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Pred.
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Mismatches
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Mismatches
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A; Gene: DR1031
A; Map position: C; Superfamily: (
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A; Reference number: A75250; MUID:20036896
A;Accession: H75446
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A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; la;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483
A;Accession: G84353
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G84353
G84951
G94951
hypothetical protein Vng2034h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                            (S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: H75446
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do
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Best Local Similarity
Watches 5; Conserve
                                                                        A; Cross-references: GB: AE001954; A; Experimental source: strain R1 C; Genetics:
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A; Residues: 1-353 <WHI>
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A;Note: sequence extracted from NCBI backbone (NCBIN:117052, NCBIP:117053)
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox: nucleus; transcription regulation
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A; Residues: 1-273 <BEA>
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A;Accession: B48820
A;Status: preliminary
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A; Residues: 1-274 <STO>
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5; Conserv
  (S)-2-hydroxy-acid oxidase;
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                                                                                                                     GB:AE000513; NID:g6458751;
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59;
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C.; M
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                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein TC0328 [imported] - Chlamydia muridarum (strain Ni ;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: D81715 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H; C:; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sa Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
                                                                                                                                                                                                      C;Genetics:
A:Gene: TC0328
                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-374 <TET>
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
Search completed: October 24, Job time: 8.39344 secs
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A;Accession: D81715
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ALIGNMENTS

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-EL TOR N16961 / SEROTYPE 01; MEDLINE-20406833; PubMed=10952301; Heldelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Gill S.R., Nelson K.E., Read T.D., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,	ramamoro k., Do V.G.K.F., Xu M., 11da T., Miwatani T., Albert M.J., Honda T.; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.	. Lett. 117:197-202(1994). N.A. 0139-BENGAL; Of Control of the	SEQUENCE FROM N.A. STRAIN-4260B / SEROTYPE 0139; MEDLIND-94237453; PubMed-8181723; Lebens M., Holmgren J.; "Structure and arrangement of the cholera toxin genes in Vibrio cholerae 0139.";	SEQUENCE FROM N.A. STRAIN-EL TOR 2125; Dams E., de Wolf M., Dierick W.; Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.	[2] SEQUENCE FROM N.A. STRAIN-EL TOR 2125; MEDLINE-84068199; PubMed-6646234; Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F., de Wilde M.; "Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development."; Nature 306:551-557(1983).	(1) SEQUENCE FROM N.A. MEDLINE-84061784; PubMed-6315707; MEDLINE-84061784; PubMed-6315707; Lockman H., Kaper J.B.; "Nucleotide sequence analysis of the A2 and B subunits of Vibrio cholerae enterotoxin."; Ch. Biol. Chem. 258:13722-13726(1983).	LT 1 VIBCH VIBCH STANDARD; PRT; 124 AA. PO1556; Q9JQ02; 21-JUL-1986 (Rel. 01, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cholera enterotoxin, beta chain precursor. CTXB OR TOXB OR VC1456. Vibrio cholerae. Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. NCBI_TaxID-666;

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Salzberg
Fraser C.
                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (see or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                     Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by Protein Sci. 6:1516-1528(1997).
-I- FUNCTION: THE BETA CHAIN AGGREGATE (B
                                                                                                                                                                                                                                                                                                                                                                                                                            "The 2.4 A crystal structure choleragenoid.";
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[7]
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MEDLINE-97376625; PubMed-9232653;
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MEDLINE=94272319; PubMed=8003954;
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J. Biol. Chem.
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(FROM THE SAME PRECURSOR MOLECULE), 1
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1XPB; 01
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structure of the beta chain
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Heat-labile
                                                           SEQUENCE FROM N.A.
STRAIN-ISOLATE H74-114;
STRAIN-S5156481; PubMed=3884513;
MEDLINE-85156481; PubMed=3884513;
Leong J., Vinal A.C., Dapalas W.S.;
"Nuclectide sequence comparison between cistrons from Escherichia coli of human Infect. Immun. 48:73-77(1985).
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                 Yamamoto T., Tamura T. "Overlapping genes in from Escherichia coli
                                    STRAIN-ISOLATE H10407;
MEDLINE-83114628; PubMed-6759877;
                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
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SEQUENCE FROM N.A.
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124 AA;
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           ura T.A., Yokota T., Tes in the heat-labile coli human strain."; 188:356-359(1982).
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STRAIN-ISOLATE H10407;

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RESULT 3
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MAKKOVIC-Calogovic D., Loregian A., D'Acunto M.R., Battistutta k.,

Tossi A., Palu G., Zanotti G.;

"Crystal structure of the B subunit of Escherichia coli heat-labile
"Crystal structure of the B subunit of escherichia coli heat-labile
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EMBL; S60731; AAC60441.1; -.
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EMBL; X83966; CAA58800.1; -.
PDB; ILTR; 23-MAR-99.
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Domenighini M., Pizza M., Jobling M.G.,
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FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli F "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).

-I- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
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MEDLINE-91238966; PubMed-2034287;
Sixma T.K., Pronk S.E., Kalk K.H., War
Witholt B., Hol W.G.J.;
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MEDLINE-87137303; Pub
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Leong J., Vinal A.C., Dallas
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"Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
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MEDLINE-81074965; Pu
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Bacteria; Proteobacteria;
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from E. coli.";
Nature 351:371-377(1991).
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"Refined structure of Escherichia
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"A functional interaction
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230:890-918(1993).
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P42238;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
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MEDLINE-95219079; PubMed-7704254; Ogawa K.-I., Akagawa E., Nakamura K., Ya "Determination of a 21548 bp nucleotide degrees region of the Bacillus subtilis Microbiology 141:269-275(1995).
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or send an email t
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1HTL;
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B26946; QLECEB.
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Pro; IPR001835; Enterotoxin_B.
PF01376; Enterotoxin_B; 1.
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M17101; AAA23973
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31-JAN-94.
31-JAN-94.
31-JAN-94.
07-JUL-97.
16-JUN-97.
03-DEC-97.
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31-JAN-94.
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Pred. No. 0.2
0; Mismatches
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                                                                      Bacillus
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 Q.
              chromosome.
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Best Local :
                                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan
Parson J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R
sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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SEQUENCE
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EMBL; 299105; CAB12043.1; -
HSSP; P42206; 1BQG.
SubtiList; BG11161; gudD.
InterPro; IPR001354; MR_MLE
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                          Nature 368:32-38
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994
01-MAR-2002
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Wohldman P
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CATALYTIC ACTIVITY: D-glucarate - 5-dehydro-4-deoxy-D-glucarate H(2)o.
PATHWAY: FIRST STEP IN GLUCARATE CATABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinformatics Institute.
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LACTONIZING
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PF02746; MR_MLE_N;
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MILARITY: BELONGS TO PEPTIDASE FAMILY S28 (SERINE PROTEASE)
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(Rel. 41, Last annotation update)
rine protease ZKI12.1 precursor (EC 3.4.-.-).
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TY: BELONGS TO THE MANDELATE RACEMAI
ING ENZYME FAMILY. GLUCD SUBFAMILY.
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MEDLINE=99192810; PubMed=10092850;
Rusd A.A., Ikejiri Y., Ono H., Yon
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30-MAY-2000 (Rel. 39, Last
30-MAY-2000 (Rel. 39, Last
Protein-arginine deiminase
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ittes requires a license agreement (see http://www.isb-sib.ch/an
send an email to license@isb-sib.ch).
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FUNCTION: CATALYZES THE DEIMIN
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  (EC 3.5.3.15) (Peptidylarginine
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Best Local
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InterPro; IPR004303; PAI
Pfam; PF03068; PAD; 1.
Hydrolase; Calcium-bind;
CA_BIND 505 516
SEQUENCE 666 AA; 744;
                                                                                                                                                                                                                                                                                                                                                                                                               [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; K
Mammalia; Eutheria; K
NCBI_TaxID=10090;
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Q61045; P70183;
01-NOV-1997 (Rel. 3
15-JUL-1999 (Rel. 3
16-OCT-2001 (Rel. 4
Submitted [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single-minded suggest possible roles
the pathogenesis of Down syndrome.";
Mol. Cell. Neurosci. 7:1-16(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ran C.-M., Kuwana E., Bu
Jenkins N.A., Crews S.,
Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SWISS WEBSTER;
MEDLINE-97020303; Pub
                                                                                                                                                                                                                                                                                       Chrast R., Scott H.S., Chen H., I Wang Y., Shimizu N., Antonarakis Genome Res. 7:615-624(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fan C.-M., Kuwana E., Bu
Jenkins N.A., Crews S.,
Tessier-Lavigne M.;
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                                                                                                                                         Ema M., Morita M., Ikawa S., Tanaka M., I
Saijoh Y., Fujii H., Hamada H., Kikuchi
"Two new members of the murine Sim gene
repressors and show different expression
                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO C-TERMINUS.
MEDLINE=97343329; PubMed=9199934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single-minded
                                   Hosoya T
                                                    SEQUENCE FROM STRAIN=129/SV;
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embryogenesis.";
                                                                                                                                                                                                                MEDLINE=96413339; PubMed=8927054;
                                                                                                                                                                                                                                    STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                            Unpublished results,
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5; Conserv
                (APR-1998)
                                                                                                       Biol.
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505 516
666 AA; 74476 M
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                                                                                                         16:5865-5875(1996)
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38,
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E., Bulfone A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8875433;
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Rodentia;
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71.48;
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EF-HAND (POTENTIAL)
                EMBL/GenBank/DDBJ
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S S.E.;
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40;
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Y., Fujii-Kuriyama Y.;
family are transcriptional
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Rubenstein
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EMBL; D79209; BAA11467.1; -
EMBL; AB013491; BAA28270.1; JOINED
EMBL; AB013484; BAA28270.1; JOINED
EMBL; AB013485; BAA28270.1; JOINED
EMBL; AB013486; BAA28270.1; JOINED
EMBL; AB013487; BAA28270.1; JOINED
EMBL; AB013489; BAA28270.1; JOINED
EMBL; AB013489; BAA28270.1; JOINED
EMBL; AB013489; BAA28270.1; JOINED
EMBL; AB013499; BAA28270.1; JOINED
                                                                                                                                                                                                                                                                                       Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
PRINTS; PR00785; NCTRNSLOCATR.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFORATOR PROTEIN.

J. Biol. Chem. 272:4451-4457(1997).

-I.- FUNCTION: TRANSCRIPTIONAL FACTOR THAT MAY HAVE PLEIOTROPIC EFFECTS DURING EMBRYGENESIS AND IN THE ADULT.

-I.- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODIMER OF SIMI AND ARMY.

-I.- TISSUE SPECIFICITY: DETECTED IN LUNG, SKELETAL MUSCLE AND KIDNEY.

DURING FETAL DEVELOPMENT IT IS FOUND IN THE CNS, DEVELOPING KIDNEY. MESODERMAL AND ENDODERMAL TISSUES, INCLUDING DEVELOPING SOMITES, MESODEPHRIC DUCT, AND FOREGUT.

-I.- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                      CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                          DNA_BIND
                                                                                                                                                                                                                                       Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probst M.R., Fan C.M., Tessier-Lavigne M., Hankinson O.; "Two murine homologs of the Drosophila single-minded protein that
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interact with the mouse aryl hydrocarbon receptor
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MEDLINE-97172525; PubMed-9020169;
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ERPGSQH 429
                         EVPGSQH 7
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                                                   Similarity 6; Conser
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IPR001092; HLH_dim.
IPR001067; Nuctrnslocator.
IPR001610; PAC.
IPR000014; PAS.
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218
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176
322
480
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765
                                                   Conservative
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85.7%;
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P -> R (
A -> P (
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Pred. No.
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PAS 2.
H -> L (IN REF. 1).
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RESULT 9
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YH96_MYCLE
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Matches 5
                                                     CIDA_HUMAN
060543;
16-OCT-2001
16-OCT-2001
16-OCT-2001
Cell death a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21128732; PubMed-11234002;
MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Bevlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=88088878; PubMed=2447183;

Booth R.J., Harris D.P., Love J.M., We artigenic proteins of Mycobacterium gene for the 18-kDa protein.";

J. Immunol. 140:597-601(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                             CIDEA.
                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 13
                                                                                                                                                                                                                                                                                                                                             PIR; B27586; B27586.
Leproma; ML1796; -.
                                                                                                                                                                                                                                                                                                                                                                          EMBL; M19058; AAA88230.1; -. EMBL; AL583923; CAC30749.1; -.
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Barrell B.G.;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae. Bacteria; Firmicutes;
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                                                                                                                                                                                                                               2 VPGSQH 7
                                                                                                                                                                                                    VPGNQH 132
                                                                                                                                                                                                                                                        Similarity
5; Conserv
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                                                        1 (Rel. 40, Created)
1 (Rel. 40, Last sequence up
1 (Rel. 40, Last annotation
activator CIDE-A (Cell deat
                                                                                                                                                                                                                                                                                                                    l protein;
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15195 MW;
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 Craniata;
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633E68BF3FDAD0BB CRC64;
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l death-inducing/
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12;
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  Vertebrata; Euteleostomi;
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                                                           DFFA-like effector
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                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-MSB8 / DSM 3109;

MEDLINE-9287316; PubMed-10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P58009;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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InterPro; IPR003508; CAU
Pfam; PF02017; CIDE-N; J
Pfam; CAD; 1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                               IDENTIFICATION.
Medique C., Bocs S.;
Unpublished observations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical TM1158.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- FUNCTION: ACTIVATES APOPTOSIS.
-I- SUBUNIT: INHIBITED BY DFFB.
-I- SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima.
Bacteria; Thermotogales;
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MEDLINE-98232498; PubMed-9564035;
MEDLINE-98232498; PubMed-9564035;
MEDLINE-98232498; PubMed-9564035;
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5; Conservative
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Pred. No.
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05F704823CE71C0E
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Best Local S
Matches 5
DNA_BIND
SEQUENCE
                                                                                             "Two distal-less related homeobox-containing genes regeneration blastemas of the newt.";
Dev. Biol. 154:55-65(1992).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN REGENERATION
IN FORELIMBS, HINDLIMBS, THE TAIL, FLANK, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                  PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
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              Homeobox; DNA-binding; DNA_BIND 125 184
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93050784; PubMed=1358728; Beauchemin M., Savard P.;
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Skin;
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01-OCT-1996 (Rel. 34, Last sequence update
01-OCY-1997 (Rel. 35, Last annotation update
01-NOV-1997 (Rel. 35, Last annotation)
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273 AA;
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240 AA; 27773 MW;
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                         Developmental protein;
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Query Match Best Local S Matches 5

h 79.5%; Similarity 71.4%; 5; Conservative

Score 31; DB Pred. No. 26; 1; Mismatches

1:

Length 273;

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EVPGSQH

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DLX3_
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DLX3_PLEWA
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Best Local S
Matches 5
                   Q90229;
01-NOV-1997
01-NOV-1997
30-MAY-2000
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01-NOV-1997
15-JUL-1998
Distal-LESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMBME
           Homeobox
                                                                 DLX3_AMBME
                                                                                                                                                                                                                                                                     PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=96391186; PubMed=8798159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                            Homeobox; DNA-binding; Developmental protein; Nuclear protein DNA_BIND 126 185 HOMEOBOX. SEQUENCE 274 AA; 30607 MW; 94148553BA80B8C8 CRC64;
                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                       EMBL; U49645; AAA98645.1; HSSP; P22808; 1NK3.
                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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Pleurodeles waltlii (Iberian ribbed newt).

Pleurodeles waltlii (Iberian ribbed newt).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8319;
                                                                                                                        189
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                                                                                                                                                                  Local Similarity les 5; Conserv
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                                                                                                                       EVPGMEH
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                                                                                                                                            EVPGSQH 7
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                                                                                                                                                                                                                                                                                                        PF00046;
         protein
                                                                                                                                                                                                                                                                                                                IPR000047; HTH_repressr.
IPR001356; Homeobox.
                   (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequence up)
(Rel. 36, Last annotation)
like protein DLX-3.
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                        homeobox;
                                                                  STANDARD;
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                   35, Created)
35, Last sequence up
39, Last annotation
                                                                                                                                                                             79.58;
                                                                                                                                                                                                                                                                                                               Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                 ; Score 31; DB
; Pred. No. 26;
1; Mismatches
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                      update)
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                                                                                                                                                                                       Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COT2_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Best Local
                                                           Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: REGULATION OF THE APOLIPPEROTEIN AI GENE:
BINDS TO DNA SITE A (BY SIMILARITY).
-i- SUBGUNIT: BINDS DNA AS AN HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OOT2_BOVIN STANDARD: PRT; 414 AA. (97TRT; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) COUP transcription factor 2 (COUP-TF2) (COUP-TF NR2F2 OR TFCOUP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEODOX; DNA-binding; Developmental protein; Nuclear protein.
DNA_BIND 126 185 HOMEOBOX.
SEQUENCE 280 AA; 31200 MW; 0F8183097ABAC791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use as long as long as its content use as long as l
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-I- SUBCELLULAR LOCATION: NUCLEAR (Potential).
-I- SIMILARITY: BELONGS TO THE DISTAL-LESS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031, HTHREPRESSR.
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ambystoma mexicanum
Eukaryota; Metazoa;
Amphibia; Batrachia
                                                                                                                                                                                                                                                                                   Walther N.;
                                                                                                                                                                                                                                                                                                                 TISSUE=Corpus luteum;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
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InterPro; IPR001356;
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                             SUBFAMILY.
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5; Conser
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Chordata; Craniata; Vertebrata; Euteleostomi;
; Caudata; Salamandroidea; Ambystomatidae;
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71.4%;
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the role of
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26;
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Distal-less and
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                                                                      RECEPTORS
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                                                                      FAMILY.
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COT2_HUMAN
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GN NR2F2
OC ELKER
OC ELK
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Matches 6
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InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00198; STRDHORMONER.
PRINTS; PR00047; STROLDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00430; HOLI; 1.
SMART; SM0039; ZDF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P24468; Q03754;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
COUP transcription factor 2 (COUP-TF2) (COUP-TF
regulatory protein-1) (ARP-1).
NR2F2 OR TFCOUP2 OR ARP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91118002; PubMed=1899293;
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between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                              Q9R646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
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Best Local S
Matches 7
Q57193 PRELIMINARY;
Q57193;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                           Microbiol. Immunol. 39:87-94(1995).
HSSP; P01556; IXTC.
InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM: PD012805; Enterotoxin_B; 1.
ProDOM: PD012805; Enterotoxin_B; 1.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9R646 PRELIMINARY; PRT; 103 AA.
Q9R646;
Q9R646;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                         MEDLINE-95303036; PubMed-7783690;
Nakashima K., Eguchi Y., Nakasone N.
"Characterization of an enterotoxin
                                                                                                                                                                                                                                                                                                                0139."
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                        Local Similarity hes 7; Conserv
                                                                                                   51
                                                                                                                              1 EVPGSQH 7
                                                                                                   EVPGSQH
                                                                                                                                                       100.0%; Score 39; DB 2; Length 103; llarity 100.0%; Pred. No. 0.53; Conservative 0; Mismatches 0; Indels
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Best Local S
Matches 7
        "Cloning and nucleotide sequence analysis of the cassette from vibrio cholerae KNIH002 isolated in Misainmurhag Hoiji 35:205-210(1999).

EMBL; AFI75708; AAD51360.1; -.

HSSP; P01556; 2CHB.
InterPro; IPRO1835; Enterotoxin_B.
Pfam; PP01376; Enterotoxin_B.
Pfam; PP01376; ENTEROTOXINB.
PRODOM; PD012805; Enterotoxin_B; 1.
PRODOM; PD012805; Enterotoxin_B; 1.
                                                                                                                                                   Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                         CTXB.
                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHOLERA ENTEROTOXIN B-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                      Signal.
SIGNAL
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  SEQUENCE
                                                                                                                       SEQUENCE FROM N.A.
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Bacteria; Proteobacteria;
                                                                                                    Shin H.J., Park Y.C.,
                                                                                                              STRAIN-KNIH002;
                                                                                                                                           NCBI_TaxID=666;
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STRAIN-CLASSICAL BIOTYPE
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MEDLINE-91355224; PubMed-1883840;
Dams E. De Wolf M., Dierick W.;
Nucleotide sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00772; ProDom; PD012805;
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s; PR00772; ENTEROTOXINB.
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C., Zhang J., Ma Q.;
em. J. 9:395-399(1993).
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13919 MW;
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Last annotation updat
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CHOLERA TOXIN B PROTEIN
D6BF83FFF7924EA3 CRC64
   23BF83FFF793E5B9 CRC64;
                                                                                                                                                      subdivision; Vibrionaceae; Vibrio.
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Q93V32;
01-DEC-2001
01-DEC-2001
01-DEC-2001
HEAT-LABILE
                                                                                                                                                                                                                                                                                     ProDom;
Signal.
SIGNAL
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Q56635;
 STRAIN=1032 (ENTEROTOXIGENIC);
MEDLINE=95091056; PubMed=7990417;
Tamura S., Asanuma H., Tomita T.,
Hattori N., Watanabe K., Suzuki Y
                                                                                                                                                                                                                                                                                                   InterPro; IPR001835; Enterotoxin_B. pfam; pf01376; Enterotoxin_B; 1. pr1NTS; pr00772; ENTEROTOXINB. proDom; PD012805; Enterotoxin_B; 1.
                         SEQUENCE FROSTRAIN=1032
                                                                SEQUENCE FROM
STRAIN=1032 (I
                                                                                                                Escherichia
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                                                                                        NCBI_TaxID=562;
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                                                                                                        Bacteria;
                                                                                                                        LTH B SUBUNIT
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13871 MW;
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18 SUBUNIT.
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and S7 (O37) from two outbrea
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Kawahara K.
T., Aizawa (
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01-JAN-1998
01-JAN-1998
01-DEC-2001
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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Vaccine 12:1083-1089(1994).
Vaccine 12:1083-1089(1994).
EMBL; AB011677; BAA25726.1; -.
                                                                     SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A);
Caccol T., Adams D.O.;
Caccol T., Adams D.O.;
                                   Cassol T., Adams D.O.;
"Cloning of a grape glutathione reductase cDN/
expression during berry development.";
submitted (AUG-1997) to the EMBL/GenBank/DDBJ
-!- COFACTOR: FAD (BY SIMILARITY).
                                                                                                                                    Vitis vinifera (Grape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                 Bhattacharyyaa T., Nandy R.K., Nair G.B.; "The entire core region of the ctx-phi (ctx-prophage) in environmental strain of V. Cholerae."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF414369; AAL09682.1; -. SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio phage CTX.
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                      HSSP;
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a trace amount of
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Pred. No.
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InterPro; IPR004099; pyr_redox_dim.
Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; pyr_redox_dim; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00461; PNDRDTASEI.
PRINTS; PR00461; PNDRDTASEI.
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FAD; Flavoprotein; Oxidoreductase.
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Q9W7D4;
                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostel; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
NCBI_TaxID=8090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Reprod. Dev. 55;31-36(2000).
EMBL; AF128818; AAD39915.1; -.
Hypothetical protein.
SEQUENCE 195 AA; 21446 MW; B90682D695729E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 21.4 KDA PROTEIN. Oryzias latipes (Medaka fish).
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SEQUENCE FROM N.A. STRAIN=ORANGE-RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-ORANGE-RED;
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Mol. Reprod.
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Systematic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20070874; PubMed=10602271;
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Pred. No.
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Pred. No.
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RESULT 11
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Best Local S
Matches 6
Q9NPO6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence of the company of the co
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Q9RJZ8;
Q1-MAY-2000 (TrEMBLrel. 1
Q1-MAY-2000 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
PUTATIVE AMIDASE.
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SEQUENCE
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Redenbach M., Kleser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
Rinashi H., Hopwood D.A.;
Rinashi H., Hopwood D.A.;
Bet of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL133210; CAB61584.1;
InterPro; IPR002502; Amidase_2.
Pfam; PF01510; Amidase_2; 1.
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Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                                      Q9NPQ6
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"Systematic identification
in medaka.";
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nes 6; Conserv
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01-DEC-2001 (TIEMBLIFE! 19, Last annotation update)
HYPOTHETICAL 31.0 KDA PROTEIN (UNKNOWN) (PROTEIN FOR
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SEQUENCE 272 AA; 31016 MW;
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Mammalia; Eutheria;
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Wambutt R., H
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Mammalia; Eutheria;
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Lundeberg J.;
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CG3837 PROTEIN.
CG3837.
Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9Y2B3 PRELIMINARY;

O9Y2B3;

O1-NOV-1999 (TrEMBLrel. 12,

O1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka-Ueguchi M., Itoh H., Oyama N., Koshioka M., Matsuoka M "Over-expression of a tobacco homeobox gene, NTH15, decreases expression of a gibberellin biosynthetic gene encoding GA 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and expression of a novel lysophospholipase which structurally resembles lecithin cholesterol acyltransferase."; Biochem. Biochem. Res. Commun. 257:50-56(1999).
EMBL; AB017494; BAA76877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1998) to the EMBL; AB016084; BAA31690.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTC16
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Sumino Y., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99194552; PubMed=10092508;
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Pfam; PF00671; Fe_Asc_oxidored; 1.
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6; Conser
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AA; 4
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Pred. No.
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Pred. No.
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         Tracheata; Hexapoda; Insecta;
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RA Ballew R.M., Basu A., Mun. B., Andrews Flaumoch C., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bensley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bensley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Devangelista C.C., Perrac C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.B., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Raillams R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RT Type genome sequence of Drosophila melanogaster.";
DR EMBL, AE003706; AAF55118.1;
DR EMBL, Sasser Frandon S., COSSOPhila melanogaster.";
DR EMBL, AE003706; AAF55118.1;
                                                                                                                                         Matches
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Best Local
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B. W. Been A. Barradaler T. Barrattasoch T. Barrattasoch
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NCBI_TaxID-7227;
[1]
                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0038279; CG3837. InterPro; IPR000494; EGFR_L.
                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                    EVPGSQH
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818
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                                                                                                                                                                   84.68;
                                                                                                                              Score 33; DB 5; L
Pred. No. 1.1e+02;
2; Mismatches 0;
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F6562A64E72E7B21 CRC64;
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G., Zhao Q., Zheng L.,
S., Zhu X., Smith H.O.,
                                                                                                                                                                                                       Length 868;
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Maximum DB
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
  GenCore version (c) 1993 - 2000
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ILTR_HUMAN
GABT_HUMAN
A37C_DROME
AMH2_HUMAN
RFXS_HUMAN
SR68_CAEEL
SIM1_HUMAN
SIM1_HUMAN
THI1_SCHPO
AHR_MOUSE
PLD_TOBAC
AHR_RAT
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AROC_NEUCR
IL7R_MOUSE
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T., Miwan T., Miwan T., Miwan T., Miwan Miwan T., Miwan T., Miwan T., Miwan T., Miwan T., Miwan T., Miwan H., Miwan	W.; EMBL/GenBank/DDBJ d 1723; f the cholera toxin 7-202(1944)	G.D.N.,	_	4. HUMAN 2_HUMAN 2_HUMAN C_DROME _ECOLI _BROME A_CHICK G_CORSP 3_DROME 3_DROME 3_DROME 1_AGABI 5_YEAST 5_YEAST
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"DNA sequence c
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Structural studies of receptor binding by cholera toxin mutants.

Protein Sci. 6:1515-1528(1997).

-I- FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN

BINDING TO CELL MEMBRANES.

-I- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHA

(FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN

DISULLFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF
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STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS). MEDLINE-95387394; PubMed-7658472;
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MEDLINE-78005537; PubMed-903363;

Kurosky A., Markel D.E., Peterson J.W.

"Covalent structure of the beta chain
"Covalent Structure of the Jeta Chain
J. Biol. Chem. 252:7257-7264(1977).
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X01170; AAA27573.1; -.

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X76391; CAA53976.1; -.
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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6 BETA CHAINS.
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STRAIN-ISOLATE H10407;

MEDLINE-83114628; pubMed-6759877;

MEDLINE-83114628; pubMed-6759877;

Yamamoto T., Tamura T.A., Yokota T., T

"Overlapping genes in the heat-labile
from Escherichia coli human strain.";

Mol. Gen. Genet. 188:356-359(1982).
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Germani Y., Desperrier J.M.;
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Crystal structure of the B subunit of escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       x-RAY CRYSTALLOGRAPHY (3.04 ANGSTROMS).
MEDLINE=99185101; PubMed=10085117;
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13L; J01646; AAB02982.1; -.
13L; S60731; AAC60441.1; -.
13L; X83966; CAA58800.1; -.
13; 1LTR; 23 MAR-99.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                      "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";

Mol. Microbiol. 15:1165-1167(1995).

1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN. WHICH ACTIVATES INTRACELLULAR ADENTL CYCLASE.

-1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                             MEDLINE-91238966; PubMed-2034287; Sixma T.K., Pronk S.E., Kalk K.H., Witholt B., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants
Escharichia coli and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence comparison between cistrons from Escherichia coli of human Infect. Immun. 48:73-77(1985).
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"Amino acid sequence homology between cholera coli heat-labile toxin.";
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15-JUL-1998 (Rel. 36, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B,
                                                                                                                                                                                    MEDLINE-95349400; PubMed-7623669;
Domenighini M., Pizza M., Jobling M.G.,
"Identification of errors among databas
                                                                                                                                                                                                                                                                                                                                                                                          Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.: "Refined structure of Escherichia coli heat-labile close relative of cholera toxin.";
J. Mol. Biol. 230:890-918(1993).
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MEDLINE-87137303; Publ
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MEDLINE-85156481; Pu
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MEDLINE-81074965; Pu
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hiller L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
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                                       use by non-profit institutions as lon modified and this statement is not removentaties requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                              STRAIN=BRISTOL N2;
MEDLINE=94150718;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: FIRST STEP IN GLUCARATE CATABOLISM.
SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCONATE
LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).

CATALYTIC ACTIVITY: D-GLUCARATE = 5-DEHYDRO-4-DEOXY-D-GLUCARATE
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                L14324;
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bean Bioinformatics Institute.
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; AAA28181.1;
S44886.
                                                                                                                                                                                                                    Watson A., Weinstock L., Wilkinson-Sproat
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28,
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KDA
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71.4%;
                                                                                                                                                                                       nucleotide sequence from chromosome III of C.
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Last annotation update)
PROTEIN ZK112.1 IN CHROMOSOME
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Pred. No.
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                                                        (See http://www.isb-sib.ch/announce,
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27;
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MBL outstation -
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SEQUENCE
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between
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Hypothetical protein.
SEQUENCE 534 AA; 59221 M
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Q9Z183;
                                                                                                                                                             the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DEIMINASE
                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                MEDLINE=99192810; PubMed=10092850;
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                                                                                                      Hydrolase; Calcium-binding; Multigene family.
                                                                                                                                                                                                                                                                                                   mouse.
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30-MAY-2000
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239
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
ELPGGQH 245
                  EVPGSQH 7
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                                                                                                                  MGI:1338898; Pd14
                                                                                                                          AB013850; BAA34246.1;
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5; Conserv
                                     Similarity
5; Conser
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666 ‡
                                                                                                                                                                                                                                                                                                                                        Ikejiri Y.,
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation updat
ININE DEIMINASE TYPE IV (EC 3.5.
                                     Conservative
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74476 MW;
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Rodentia;
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71
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70FAE4E7E232D34A CRC64;
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Sciurognathi; Muridae;
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RESULT

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MOUSE
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Probst M.R., Fan C.M., Tessier-Lavigne M., Hankinson
"Two murine homologs of the Drosophila single-minded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ema M., Morita M., Ikawa S., Tanaka M., N
Saijoh Y., Fujii H., Hamada H., Kikuchi Y
"Two new members of the murine Sim gene
repressors and show different expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ran C.-M., Kuwana E
Jenkins N.A., Crews
Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97029422: PubMed-8875433; Fan C.-M., Kuwana E., Bulfone A., Jenkins N.A., Crews S., Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single-minded suggest possible roles
the pathogenesis of Down syndrome.";
Mol. Cell. Neurosci. 7:1-16(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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15-JUL-1999 (Rel. 38,
30-MAY-2000 (Rel. 39,
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01-NOV-1997
                       <del>:</del>
                                                                                                                                                                                                      J. Biol. Chem. 272:4451-4457(1997).

-i- FUNCTION: TRANSCRIPTIONAL FACTOR THAT MAY HAVE PLEIOTROPIC EFFECTS
DURING EMBRYOGENESIS AND IN THE ADULT.

THE ADULT.

THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                                  translocator protein.";
J. Biol. Chem. 272:4451-4457(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fan C.-M., Kuwana E., Bulfone A.,
Jenkins N.A., Crews S., Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SWISS WEBSTER;
MEDLINE=97020303; PubMed=8812055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     embryogenesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 7:615-624(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished results,
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                                                                                                                                                                                                                                                                                                                interact with the mouse aryl hydrocarbon
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                                                           SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODIMER OF SIMI AND ARRIT.

TISSUE SPECIFICITY: DETECTED IN LUNG, SKELETAL MUSCLE AND KIDNEY.

DURING FETAL DEVELOPMENT IT IS FOUND IN THE CNS, DEVELOPING KIDNEY, MESONEBHAL AND ENNODERWAL TISSUES, INCLUDING DEVELOPING KIDNEY, MESONEBHAIC DOUT, AND FOREOUT.

SOMITES, MESONEBHAIC DOUT, AND FOREOUT.

SOMITES, MESONEBHAIC DOUT, AND FOREOUT.
                    TRANSCRIPTION FACTORS. SIMILARITY: CONTAINS 1
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Rodentia;
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S., Puelles L.,
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1 Y., Fujii-Kuriyama Y
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PFam; PF00989; PAG; 2.
PRINTS; PR00785; NCTRNSLOCATR.
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Developmental protein; Neurogenesis; Nuclear protein; Nuclear protein; Nuclear protein; Nuclear prot
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Matches 6
                                                                                                           SEQUENCE FROM N.A.
MEDLINE-88088878; PubMed-2447183;
Booth R.J., Harris D.P., Love J.M., W
Pantigenic proteins of Mycobacterium
gene for the 18 kDa protein.";
J. Immunol. 140:597-601(1988).
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01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 15 KDA PROTEIN IN 18 KDA ANTIGEN 3'REGION.
                                                                                                                                                                                                                                                                                                                   Actinomycetales;
NCBI_TaxID=1769;
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B1A7F7DA8578CD17 CRC64;
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PIR; B27586; B:
Hypothetical pi
SEQUENCE 137
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
CELL DEATH ACTIVATOR CIDE-A (CELL DEATH-INDUCING
                                                                                                                                                                                                                                                                                               EMBL; AF0413
MIM; 604440;
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Mammalia; Eutheria;
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114
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ci T., Chen S., Wu X., Nunez G.;
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DLX3_PLEWA
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                         Eukaryota;
Amphibia;
                                                                                                                                                                                                              01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                  091284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox; DNA-binding; Developmental protein; Nuclear protein.
DNA_BIND 125 184 HOMEOBOX.
SEQUENCE 273 AA; 30654 MW; B356D01233061F2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00024; HOMEOBÓX.
PRINTS; PR00031; HTHREPRESSR.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X63531;
HSSP; P02836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beauchemin M., Savard P.,
"Two distal-less related homeobox-containing genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Notophthalmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53770;
01-OCT-1996
SEQUENCE FROM N.A
                                                                      Pleurodeles
                                                                                                                                                                                        DISTAL-LESS
                                                                                                                                                                                                                                                          01-NOV-1997
                                                                                                                                                                                                                                                                                                        DLX3_PLEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regeneration blastemas of the newt.";
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                                           NCBI_TaxID=8319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93050784; PubMed=1358728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSP; P02836; 1HDD.
InterPro; IPR000047; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        188 EVPGMEH 194
                                                                                                                                        leurodeles waltlii (Iberian ribbed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN FORELIMBS, HINDLIMBS, THE TAIL, FLANK, IMPARTY: BELONGS TO TAIL BELONGS THE TAIL, FLANK, SIMILARITY: BELONGS TO TAIL BELONGS TO TAIL BELONGS TO THE TAIL BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Biol. 154:55-65(1992).
SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001356;
                                                                                            Batrachia;
                                                                                                                    Metazoa;
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(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
OTEIN DLX-3 (BOX-4) (NVHBOX-4).
                                                                                                                                                                                      (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 36, Last annotation updat
LIKE PROTEIN DLX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA45094.1;
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                  Chordata;
                                                                                            Caudata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                            Salamandroidea;
                                                                                                                    Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                        newt)
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L, FLANK, AND
                                                                                                                                                                                                                                                                                                        274 AA
                                                                                                                                                                                                            update)
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26;
                                                                                                                    Vertebrata; Euteleostomi;
                                                                                            Salamandridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 273;
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BRAIN AS WI
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RESULT DE RESULT DIL X3_AM ID DI AC Q9 DT 011 DT 012 DT 01
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Best Local
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Q90229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND SEQUENCE
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97108743; PubMed-8951064;
Mullen L.M., Bryant S.V., Torok M.A., Blumberg
Mullen dependency of regeneration: the role of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMBME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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"A Distal·less-like gene is induced in the regener
nervous system of the urodele Pleurodeles waltl.";
Mech. Dev. 56:209-220(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMEOBOX PROTEIN
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PRINTS; PR00031; HTHREPRESSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ambystoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ambystoma mexicanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox; DNA-binding; Developmental protein; Nuclear DNA_BIND 126 185 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

DEVELOPMENTAL STAGE: EXPRESSED IN THE REGENERATING SPINAL CORD
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274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n (Axolotl).
Chordata;
h; Caudata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30607 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%;
71.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94148553BA80B8C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 274;
                                                                                                                                                                                                                                                                                                           B., Gardine
Distal-less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                           Gardiner D.M.;
tal-less and FGF
                                                                                                                                                                                                          HOMEOBOX
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                                                                                                   EMBL outstation
                                                                                                         a collaboration -
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L outstation -
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Best Local
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COUP TRANSCRIPTION FACTOR 2 (COUP-TF2) (COUP-TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
COT2_E
                                                                   Pfam; PF00104; hormone_rec; 1. pfam; PF00105; zf-C4; 1. PRINTS; PR00047; STROIDFINGER. PRINTS; PR00398; STRDHORMONER
                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REGULATION OF THE APOLIPOPROTEIN AI GENE TRANSCRIP BINDS TO DNA SITE A (BY SIMILARITY).
-!- SUBUNIT: BINDS DNA AS AN HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR.
 Zinc-finger.
DOMAIN
                          Transcription regulation;
                                       PRINTS; PR01282; COUPTNFACTOR;
PROSITE; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                          InterPro; IPR000536; -.
InterPro; IPR001628; -.
InterPro; IPR001723; -.
InterPro; IPR003068; -.
                                                                                                                                                                                  EMBL; AJ249441; CAB55624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR2F2 OR TFCOUP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEODOX; DNA-binding; Developmental protein; Nuclear protein DNA_BIND 126 185 HOMEOBOX. SEQUENCE 280 AA; 31200 MW; 0F8183097ABAC791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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HSSP; P02836;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                   STROIDFINGER.
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71.4%;
                        DNA-binding;
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EMBL; U60477; AAB0947 EMBL; M62760; AAA2147 PIR; A37133; A37133. HSSP; P19793; ZNLL.

TRANSFAC;

T00045;

EMBL; M64497; AAA86429.1; EMBL; U60477; AAB09475.1; EMBL; M62760; AAA21479.1;

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Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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P24668; Q03754; Q03754;
P24668; Q03754;
P24668; Q03754;
P24668; Q03754; Q03754;
P24668; Q03754; Q03754;
P24668
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ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: REGULATION OF THE APOLIPOPROTEIN BINDS TO DNA SITE A.
-I- SUBUNIT: BINDS DNA AS AN HOMODIMER.
-I- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ladias J.A.A., Karathanasis S.K.; "Regulation of the apolipoprotein AI the steroid receptor superfamily."; Science 251:561-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Expr. 1:207-216(1991).
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MEDLINE=92314709; PubMed-1820218;
Wang L.H., Ing N.H., Tsai S.Y., O'Malley B.W.,
"The COUP-TFs compose a family of functionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91118002; PubMed-1899293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NR2F2 OR TFCOUP2 OR ARP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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C24CB023C8A27F57 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
ZN_FING
ZN_FING
                       InterPro;
InterPro;
                                                                                                                                                                                                                                 Jonk L.J.C., de Jonge M.J., Pals C.E.G.M., Wissink S., Vervaart J.M.A., Schoorlemmer J., Kruijer W.; "Cloning and expression during development of three murine members the COUP family of nuclear orphan receptors."; Mech. Dev. 47:81-97(1994).

-!- FUNCTION: REGULATION OF THE APOLIPOPROTEIN AI GENE TRANSCRIPTIC BINDS TO DNA SITE A (BY SIMILARITY).

-!- SUBUNIT: BINDS DNA AS AN HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                            EMBL; X76653; CAA54096.1
HSSP; P19793; 2NLL.
MGD; MGI:1352452; Nr2f2.
InterPro; IPR000536; -.
                                                                                                           use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COUP TRANSCRIPTION FACTOR 2 (COUP-TF2) (COUP-TF
REGULATORY PROTEIN-1) (ARP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COT2_MOUSE
P43135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00031; NUCLEAR_RECEPTOR; 1. Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-95034311; PubMed-7947324;
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                  NR2F2 OR TFCOUP2 OR ARP1 OR ARP-1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVPGSQ 6
                                                                                                                                                                                                            SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
NR2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVPGSQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00104; hormone_rec; PF00105; zf-C4; 1.
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6; Conserv
                        IPR001628;
IPR001723;
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IPR001723;
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337
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                                                                                    CAA54096.1;
hormone_rec;
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                                                                                                                                                                                                                        BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
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45571
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NUCLEAR R
C4-TYPE.
C4-TYPE.
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C24CB2E8C8A27E8C CRC64;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                      (See http://www.isb-sib.ch/announce/
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MBL outstation -
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commercial
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Best Local
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       Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Prinrs; PR00105; zf-C4; 1.
PRINTS; PR00047; STROIDEINGER.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR001282; COUPTNEACTOR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COT2_RAT 009018;
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ZN_FING
ZN_FING
DOMAIN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COUP TRANSCRIPTION FACTOR 2 (COUP-TF2) (COUP-TF II) (APOLIPOPROTEIN AI
REGULATORY PROTEIN-1) (ARP-1) (OVALBUMIN UPSTREAM PROMOTER BETA
                                                                                                    EMBL; AF003944; AAB61297.1; InterPro; IPR000536; -. InterPro; IPR001628; -. InterPro; IPR001723; -.
                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    use
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the European Bioinformatics Institute.
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PRINTS; PRO0398;
PRINTS; PRO1282;
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                                                                                                                                                                                                                                                                                                                                                      Boutin
                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pituitary;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR RECEPTOR) (COUPB).
NR2F2 OR TFCOUP2 OR ARP1.
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                                                                                                                                                                                                                                                                    mitted (MAY-1997) to the EMBL/GenBank/DDBJ d
FUNCTION: REGULATION OF THE APOLIPOPROTEIN
BINDS TO DAN SITE A (BY SIMILARITY).
SUBUNIT: BINDS DNA AS AN HOMODIMER (BY SIMI
SUBCCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE
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                                                                                                                                                                                                                                                          NR2 SUBFAMILY.
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and this statement
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        DNA-binding; Nuclear protein;
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C4-TYPE.
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IMPORTANT FOR DIMERIZATION
CB35C021B3127A99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; | Sciurognathi; Muridae;
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Best Local S
Matches 6
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Pfam; PF01264; Chorismate_synt; 1.

Pfam; PF01264; Chorismate_synt; 1.

PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.

PROSITE; PS00788; CHORISMATE_SYNTHASE_3; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

Lyase; Aromatic amino acid biosynthesis; Oxido
Multifunctional enzyme.

NP_BIND 260 291

NADPH (POTENTIAL)

SEQUENCE 432 AA; 45967 MW; 201A0B525C406FC
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Reurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomy

Eukaryota; Fungi; Ascomycota; Pezizomy
                                                                                                                                                                                                                                                                                                                                                                       EMBL; U25818; AAC49056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Biol. Chem. 270:20447-20452(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of a heterologously bifunctional chorismate synthase/flavin reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95386486; PubMed=7657620; Henstrand J.M., Amrhein N., Schmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).

SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
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  EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration
                                             Similarity
6; Conserv
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                                           ; Score 31; DB; Pred. No. 41; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME THAT POSSESSES EDUCTASE ACTIVITY, IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmid J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB Pred. No. 40; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE.
                                                                                                                                                              NADPH (POTENTIAL).
201A0B525C406F0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT FOR DIMERIZATION 5AA05165DD3F675A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLN.
NUCLEAR RECEPTOR-TYPE.
                                                                     DB
41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;

    Oxidoreductase;

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                                                                                        Length 432;
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                                                                                                                                                                CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORISMATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed from Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
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                                               Gaps
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                                               0;
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В
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                                                                                                                                                                             RESULT 18
IL7R_MOUSE
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                                                               Query Match
Best Local
                                                     Matches
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MGD; MGI:96502; II7r.
InterPro; IPR000950; --
InterPro; IPR001777; --
InterPro; IPR002465; --
                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-90199875; PubMed-2317865; Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A. Goodwin R.G., Cosman D., Dower S.K., March C.J., Namen A.E., "Cloning of the human and murine interleukin-7 receptors: demonstration of a soluble form and homology to a new rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL7R_MOUSE
P16872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    superfamily.
Cell 60:941-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                  Pfam; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMM
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: SPLEEN; THYMUS; AND ETAL LIVER.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29697; AAA39304.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;

    -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-7.

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 47
                                                    Local Similarity
les 6; Conser
                         ш
 EVDGSQH
                         EVPGSQH
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                                                                                                                                                                                                                                                                                                     PS01355;
                                                                                                                                                                                                                                                                                         Transmembrane;
                                                     Conservative
                          7
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459
239
264
459
459
189
189
117
177
282
51704
                                                                                                                                                                                                                                                                                                    HEMATOPO_REC_S_F1; 1.
                                                               79.5%;
85.7%;
                                                                                                                                                                                                                                                                                       Glycoprotein; Phosphorylation; Signal.
                                                                                                                        ₩.
                                                    Score 31; DB pred. No. 44; 0; Mismatches
                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PHOSPHORYLATION (BY PKC) (POTENTIAL)
                                                                                                                                                                                           SER/THR-RICH.
                                                                                                                                                                                                        CYTOPLASMIC (POTENTIA FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                            INTERLEUKIN-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ong as its content is in
                                                                               DΒ
                                                                                                                                                                                                                      (POTENTIAL).
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                                                                               1;
                                                                                                                                                                                                                                                              RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                              Length 459;
                                                                                                                  CRC64;
                                                                                                                                                                                                                                                              ALPHA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMMA
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (
01-OCT-2000 (
01-OCT-2000 (
PROBABLE RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P77989;
15-DEC-1998
15-DEC-1998
15-DEC-1998
MEDIJURE-20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; (ACT_SITE ACT_SITE SEQUENCE ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as long as its content use as long as lo
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                                                                                                                                                                                                                                                                                                                                                                                                    KPTA_PSEAE
Q91778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00703; Glyco_hydro_2; 1.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                             NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum). Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA-GALACTOSIDASE
LACZ OR LACA.
                                                                                                                                                  STRAIN-PAOL;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                               KPTA OR PA0054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| ||
| 346 EIPGWQH
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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453
743
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                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
A 2'-phosphoTransfErase (EC
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33223
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(Rel. 37, Last annotation
OSIDASE (EC 3.2.1.23) (LAC
                                                                                                                                                                                                                                                                          aeruginosa
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85796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.5%;
71.4%;
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                                                                                                                                                                                                                                                    gamma
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NUCLEOPHILE (BY SIMILARITY).
; FE011FF517E51DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 72;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                    subdivision;
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                                                                                                                                                                                                                                                                                                                   ion update)
(EC 2.7.-.-).
                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                    Pseudomonadaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 743;
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                                          Yuan Y.,
Lim R.M.,
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;

RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA McDonald L., Utterback T.R., Malek J.A., Phillips C.A., Richardson D.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

RT genome sequence of Thermotoga maritima.";

RL Nature 399:323-329(1999).

CC --- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

--- OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9X1I2;
30-MAY-2000
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                       This
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                                                                                                      RNA(N):

RNA(N):

SUBUNIT: THE ENZYME CONSISTS OF ENZYME WHICH IS COMPOSED OF 2 AI BETA CHAIN (BY SIMILARITY).

DOMAIN: THE AMINO-TERMINAL PORTICOLOGICAL PORTING CORE RNAP, WHEREAS THE C. TERMINAL CORE.
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                                                              TRANSCRIPTIONAL REGULATORS SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                 CATALYTIC
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                       SWISS-PROT
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Best Local
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P28777;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE),
ARO2 OR YGL148W.
                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                         TIP1, MRF1 genes and six new open reading frames.";

Yeast 13:177-182(1997).

Yeast 13:177-192(1997).

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Transferase; Transcription; DNA-directed RNA polymerase.
SEQUENCE 336 AA; 38600 MW; E361EED8D4408CF2 CRC64;
                                                                           entities requires
                                                                                                                              use
                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.; "The sequence of a nearly unclonable 22.8 kb segment on the left arm chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A, TIP1, MRF1 genes and six new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of the ARO2 gene, cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones D.G.L., Reusser U., Braus G.H.;
"Molecular cloning, characterization and analysis of the regulation
of the ARO2 gene, encoding chorismate synthase, of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
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tent is in
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RESULT 23
IL7R_HUMAN
ID IL7R_H
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Best Local S
Matches 5
                                                                                                                                                                                                                     This SWI
                                                                                    PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90199875; PubMed=2317865; Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A. Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., "Cloning of the human and murine interleukin-7 receptors: demonstration of a soluble form and homology to a new rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILTR_HUMAN STANDARD; PRT; 459 AA.
P16871;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA) (CDW127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
PIR; §
SGD; §
                                                                                                                                                                                                                                                         I: FUNCTION: RÈCEPTOR FOR INTERLEUKIN-7.
I: SUBGUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
I: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND ALSO SECRETED.
I: ALTERNARITYE PRODUCTS: 3 ISOFORMS; H20 (SHOWN HERE), H1 AND H6/SECRETED; ARE PRODUCED BY ALTERNATIVE SPLICING.
I: SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
I: SIMILARITY: BELONG TO THE CYTOKINE FAMILY OF RECEPTORS.
I: SIMILARITY: ONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
I: DATABASE: NAME-PROW; NOTE-CD guide CD127 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd127.htm".
                                                                                                                                                                                                                                                                                                                                                                                                 Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000453;
InterPro; IPR000453;
Pfam; PF01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid biosynthesis.
                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 EMBL; M29696; AAA59157.1;
                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                              superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L; X99960; CAA682
L; Z72670; CAA968
; S17246; S17246.
; S0003116; ARO2.
                                                        C34791;
146661;
                                                                                    A34791;
B34791;
                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                 60:941-951(1990).
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                                                                                    A34791.
B34791.
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CAA96860.1;
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83.3%;
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Pred.
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No.
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58;
                                                                                                                                                                                        There are no restrictions ong as its content is in
                                                                                                                                                           http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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InterPro; IPR002465; -.
Pfam; PF00041; fn3; 1.

InterPro;

InterPro;

IPR000950; -. IPR001777; -.

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Best Local S
Matches 6
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SIGNAL 1
CHAIN 21
CHAIN 21
TRANSMEM 240
DOMAIN 265
DOMAIN 128
DOMAIN 184
CARBOHYD 49
CARBOHYD 65
CARBOHYD 151
CARBOHYD 182
CARBOHYD 182
CARBOHYD 232
CARBOHYD 233
MOD_RES 283
MOD_RES 237
                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GABA AMINOTRANSFERASE)
de Biase D., Barra D., Simmaco M., John R.? Primary structure and tissue distribution aminotransferase."; Eur. J. Biochem. 227:476-480(1995).
                                                                                                                                                                                                                                                                                                                                                            _HUMAN
                                              MEDLINE=95154329; PubMed=7851425; de Biase D., Barra D., Simmaco M.,
                                                                                                        Osei Y.D., Churchich J.E.;
"Screening and sequence determination of a cDNA encoding the human brain 4-aminobutyrate aminotransferase.";
Gene 155:185-187(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                TISSUE-Brain; PubMed=7721088; MEDLINE-95237607; PubMed=7721088;
                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                             GABT_HUMAN
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                         47
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                                                                                                                                                                                                                                                    OR GABAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
6; Conserv
                                                                                   OF.
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                                                                                  368-465
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
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459
239
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                                                                                  FROM
                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 98;
5. 78;
                                                                                  N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLAVSENPESPLDCQIHRVDDTÖARDEVEGFLQDTFPQQLE
ESEKQRLGGDVQSPNCSEDVVVTPESFGRDSSITCLAGNV
SACDAPILSSRSLDCRESGKNGPHVYQDLLLSLGTTNSTL
PPFFSLQSGILTLNDVAQGQPILTSLGSNQEEAYVTMSSFY
QNQ -> VSVFGA (IN ISOFORM H1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFGRDSSLTCLAGNVSACDAPILSSSRSLDCRESGKNGPHV
YQDLLLSLGTTNSTLPPPFSLQSGILTLNPVAQGQPILTSL
GSNQEEAYVTMSSFYQNQ -> LSLSYGPVSPIIRRLMNIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY PKC) (POTENTIAL).
EMDPILITISTISFSVALLVILACVLMKKRIKDIVAPSLP
DHKKTLEHLCKERPKKULVSENPESELDCGIHRVDDIOARD
EVEGFLODTFPQQLEESEKQRLGGDVQSPNCPSEDVVVTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNQ -> VSVFGA (IN ISOFORM OFDF4C84481B8B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSNQEEAYVTMSSFYQNQ -> LS
VRNQEKI (IN ISOFORM H6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (PHOSPHORYLATION (BY PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
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                                                                                  AND
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                                                                                  PARTIAL
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                                  R.A.,
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                                                                                  SEQUENCE
                                    human
                                               Bossa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 459
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                   4-aminobutyrate
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A37C_DROME

A37C_DROME

D7 01-NOV-1990 (Rel. 16, Created)
D7 01-OCT-2000 (Rel. 40, Last sequence update)
D7 01-OCT-2000 (Rel. 40, Last annotation update)
D8 ANON-37CS PROTEIN
D8 ANON-37CS OR CS OR L(2)37CS OR CG10561.
OS Drosophila melanogaster (Fruit fly).
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                                                                                                             RESÜLT
                                                                                                                                                                                                            Query Match
Best Local
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CONFLICT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
BINDING
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disease
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PFUUAUA; amanutana, PFUUAUA; amanutana, PFUUAUA; amanutana, PFTANSTER_CLASS_3; 1.

Transferase; Aminotransferase; Pyridoxal phosphate; Transferase; Amanutana, Mitochondrion; Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CUPACION. FARMALI-!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "4-aminobutyrate aminotransferase (GABA-transaminase)
J. Inherit. Metab. Dis. 2:414-427(1999).
-I- CATALYTIC ACTIVITY: 4-AMINOBUTANOATE + 2-OXOGLUTAI
SEMIALDEHYDE + L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99336116; PubMed=10407778;
Medina-Kauwe L.K., Tobin A.J., De Meirleir L.,
Nyhan W.L., Gibson K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 137150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L32961; AAA74449.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT LYS-220.
                                                                                                                                                 22
                                                                                                                                                                       2 VPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLACENTA.

DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA, PYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                VPGSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABNORMALITIES
                                                                                                                                                                                               Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                 27
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aminotran_3;
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56557
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357
220
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113
132
191
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216
268
320
                                                                                                                                                                                                           76.9%;
83.3%;
                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                       REDUCTION IN ACTIVITY).

/FTIG+VAR_008883.

D -> H (IN REF. 2).
V -> L (IN REF. 2).
V -> G (IN REF. 2).
K -> G (IN REF. 2).
K -> G (IN REF. 2).
W -> G (IN REF. 2).
W -> G (IN REF. 2).
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RA Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hilt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Helt R.A., Sahburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Baybayni A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Abril J.F., Agbayni A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blasun D.A., Buxler H., Cadleu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Donge S., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., McCeod M.P., Kepherson D.,
RA Harklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIntosh T.C., McLeod M.P., McPherson D.L.,
RA McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Melson D.L.,
RA Rahert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.N., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.N., Saunders R.D.C., Scheeler F., Shen H.,
RA Merkultov G., Milshina N.V., Mobarry C., Morris J., Nelson H.,
RA Merkultov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkultov G., Milshina N.V., Mobarry C., Welsen D.R., Welson D.L.,
RA Rander E., Scheeler F., Zaveri J.S., Zha
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                            DEVELOPMENTAL STAGE.
MEDLINE-86165362; Pu
Spencer C.A., Gietz
                                                                                                                                                                                                                                                                         Spencer C.A.,
                                                                                                                                                                                                                                                                                                                MEDLINE=86284963;
                                                                                                                                                                                                                                                                                                                                                                                                              "Overlapping transcription units in Drosophila: sequence structure of the Cs gene."; Mol. Gen. Genet. 209:290-298(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eveleth D.D., Marsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88038375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-38 AND 102-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006;
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"A compact gene cluster in Drosophila: the unrelated compressed between duplicated amd and Ddc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-ST. LUCIA;
MEDLINE-99250256; PubMed-10231575;
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                                                                                                                                                                                                                       "Overlapping transcription
Drosophila.":
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   Analysis
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                                                                                                                                                                        322:279-281(1986)
of,
                                                                                                                                                                                                                                                                         963; PubMed=2874495;
Gietz R.D., Hodgetts R.B.;
                         362; PubMed=3007242;
Gietz R.D., Hodgett
etz R.D., Hodgetts R.B.;
transcription unit adjacent to the
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EMBL; AC5991; CAA29405.7; ALT_SEQ.
EMBL; X05991; CAA29408.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            decarboxylase gene in Drosophila melanoc
Dev. Biol. 114:260-264(1986).
-i- FUNCTION: HAS A NONVITAL FUNCTION.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TISSUE SPECIFICITY: LOW LEVELS SEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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372 QVPSSQH 378
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DEVELOPMENTAL STAGE: ABUNDANT IN EMBRYOS AND ADULTS.

CAUTION: ORE1 AND ANON-37CS TRANSCRIPTS FROM REF.3 ARE NOW KNOWN
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Similarity 71.4%;
5; Conservative
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                                                                                                                  Pred. No. 78;
1; Mismatches
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R -> L (
G -> D (
G -> S (
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R -> L (IN REF. 1).

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78;
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Search completed: July 16, 2001, 16:44:03 Job time: $462\ \text{sec}$

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From: Sent: Ford, Vanessa

Tuesday, July 02, 2002 1:30 PM

To: Subject: STIC-Biotech/ChemLib In re: 09786.648

Please search SEQ ID NOs: 2,3,4 and 5. Please run interference searches.

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8D17 Mailbox: CM1 8E12 Phone: 703.308.4735

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets or results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results; with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

Searcher: D. Schve, beg	_
Phone: 308-4292	
Location: CMI 640 3	
Date Picked Up: 7/3	
Date Completed: 7(8	
Searcher Prep/Review:	
Clerical:	
Online time: 6	_

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 4
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where app
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: Compage
WWW/Internet:

Other (specify):

